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OM protein - protein search, using sw model

Run on: July 4, 2004, 07:21:48 ; Search time 76 Seconds
(without alignments)
1197.109 Million cell updates/sec

Title: US-09-787-879c-1
Perfect score: 1688
Sequence: 1 MDSIPVLGTELTPIINGREE.....EGGWLPOETLELSGRLEQ 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1688	100.0	322	3 AAY90761	Aay90761 Human G p
2	1688	100.0	322	5 ABJ04077	Abj04077 Human G p
3	1688	100.0	322	5 AAE21296	Aae21296 Human Mrg
4	1688	100.0	322	6 ABP81750	Abp81750 Human G p
5	1688	100.0	337	5 AAU97598	Aau97598 Human G-p
6	1683	99.7	322	3 AAY90762	Aay90762 Human G p
7	1683	99.7	322	7 ADC86821	Adc86821 Human GPC
8	1663	98.5	322	3 AAB14846	Aab14846 Human nov
9	1642	97.3	322	2 AAY30159	Aay30159 Human dor
10	1598	94.7	322	2 AAY30160	Aay30160 Human dor
11	1557	92.2	302	6 ABP96695	Abp96695 Human G p
12	1405	83.2	322	2 AAY30161	Aay30161 Human dor
13	1399	82.9	304	7 ADC12766	Adc12766 Human GPC
14	1391	82.4	322	2 AAY30162	Aay30162 Human dor
15	1387	82.2	322	3 AAY97664	Aay97664 Human dor
16	1387	82.2	322	7 ADC17728	Adc17728 Human TGR
17	1383	81.9	322	4 AAG54294	Aag54294 Human GTP
18	1383	81.9	322	4 AAE12794	Aae12794 Human G p
19	1383	81.9	322	4 AAU04371	Aau04371 Human G-p
20	1383	81.9	322	5 AAE17074	Aae17074 Human GPC
21	1383	81.9	322	5 ABP95617	Abp95617 Human Mrg
22	1383	81.9	322	5 AAE21288	Aae21288 Human G p
23	1383	81.9	322	6 ABP96696	Abp96696 Human G p
24	1383	81.9	322	6 ABP59266	Abp59266 Human Dor
25	1383	81.9	322	7 ADC86445	Adc86445 Human GPC

26	1383	81.9	322	7 ABW00803	Abw00803 Human GPC
27	1379	81.7	322	2 AAY30163	Aay30163 Human dor
28	1367	81.0	322	3 AAY87663	Aay87663 Human G p
29	1367	81.0	322	5 ABJ04076	Abj04076 Human G p
30	1367	81.0	322	5 AAE21297	Aae21297 Human Mrg
31	1367	81.0	322	6 ABP96692	Abp96692 Human G p
32	1367	81.0	322	6 ABP81758	Abp81758 Human Mrg
33	1367	81.0	322	7 ADC17723	Adc17723 Human TGR
34	1361	80.6	322	7 ADC86589	Adc86589 Human GPC
35	1360	80.6	322	2 AAY30164	Aay30164 Human dor
36	1263	74.8	328	7 ADD18024	Add18024 Human G-p
37	1198	71.0	304	7 ADC12762	Adc12762 Human GPC
38	1031.5	61.1	331	5 ABB79885	Abb79885 Amino aci
39	989.5	58.6	330	4 AAG62852	Aag62852 Amino aci
40	989.5	58.6	330	4 AAG54301	Aag54301 Human GTP
41	989.5	58.6	330	4 AAY72910	Aay72910 Human IGS
42	989.5	58.6	330	4 AAB76654	Aab76654 Amino aci
43	989.5	58.6	330	4 AAU04376	Aau04376 Human G-p
44	989.5	58.6	330	5 AAE15639	Aae15639 Human G-p
45	989.5	58.6	330	5 ABB06258	Abb06258 Human G p

ALIGNMENTS

RESULT 1
AAY90761
ID AAY90761 standard; protein; 322 AA.
AC AAY90761;
XX
DT 18-AUG-2000 (first entry)
DE Human G protein-coupled receptor hH17213 SEQ ID NO:1.
KW Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
KW genetic disease; cellular function regulation.
XX Homo sapiens.
OS
PN WO200020455-A1.
XX
PD 13-APR-2000.
XX
PF 30-SEP-1999; 99WO-JP005366.
XX
PR 01-OCT-1998; 98JP-00279535.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Watanabe T, Terao Y, Matsui H;
XX WPI; 2000-303747/26.
XX N-PSDB; AAA29811.
XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
XX e.g. in determining ligands and treatment of diseases associated with
XX dysfunction of the protein.
XX Claim 1; Page 90-91; 97pp; Japanese.
XX The present sequence represents a human-derived G protein-coupled protein
XX designated hH17213, which is isolated from the human hippocampus. The G
XX protein-coupled receptor can be used for preventing, treating and
XX diagnosing genetic diseases associated with G protein-coupled protein,
XX and for regulating cellular functions. The protein can be used to prevent
XX and treat disorders associated with G protein-coupled protein gene
XX dysfunction. It can also be used to identify G protein-coupled protein
XX ligands and generating antibodies and antisera against the protein. It is
XX also useful in constructing recombinant receptor protein expression
XX systems, developing receptor-binding assay systems and screening drug
XX candidates, and can be used as a probe in the genetic diagnosis of G
XX protein-coupled protein disorders

```

XX SQ Sequence 322 AA;
Query Match 100.0%; Score 1688; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHHICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFSGHHICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
QY 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLCGLPFGIQWALFS 240
DB 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLRALQDTPE 300
DB 241 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLRALQDTPE 300
QY 301 VDEGGGWLPQETLELSGRLEQ 322
DB 301 VDEGGGWLPQETLELSGRLEQ 322

RESULT 2
ABJ04077
ID ABJ04077 standard; protein; 322 AA.
XX AC ABJ04077;
XX DT 11-OCT-2002 (first entry)
XX DE Human G protein coupled receptor hRUP37.
XX KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
XX KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
XX OS Homo sapiens.
XX PN WO200242461-A2.
XX PD 30-MAY-2002.
XX PF 26-NOV-2001; 2001WO-US044386.
XX PR 27-NOV-2000; 2000US-0253404P.
XX PR 12-DEC-2000; 2000US-0255366P.
XX PR 20-FEB-2001; 2001US-0270286P.
XX PR 20-FEB-2001; 2001US-0270286P.
XX PR 06-APR-2001; 2001US-0282032P.
XX PR 06-APR-2001; 2001US-0282356P.
XX PR 06-APR-2001; 2001US-0282356P.
XX PR 06-APR-2001; 2001US-0282365P.
XX PR 14-MAY-2001; 2001US-0290917P.
XX PR 31-JUL-2001; 2001US-0309208P.
XX PA (AREN-) ARENA PHARM INC.
XX PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX WPI; 2002-566565/60.
XX DR N-PSDB; ABT04875.
XX Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor

PT agonists or antagonists for use as therapeutic agents.
XX Claim 37; Page 75-76; 84pp; English.
XX The present invention provides the protein and coding sequences of
XX several human G-protein coupled receptors (GPCRs). These can be used in
XX the identification of candidate compounds as receptor agonists or inverse
XX agonists having applicability as therapeutic agents. The present sequence
XX is a GPCR protein of the invention
XX Sequence 322 AA;
Query Match 100.0%; Score 1688; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHHICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFSGHHICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
QY 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLCGLPFGIQWALFS 240
DB 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLRALQDTPE 300
DB 241 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLRALQDTPE 300
QY 301 VDEGGGWLPQETLELSGRLEQ 322
DB 301 VDEGGGWLPQETLELSGRLEQ 322

RESULT 3
AAE21296
ID AAE21296 standard; protein; 322 AA.
XX AC AAE21296;
XX DT 01-JUL-2002 (first entry)
XX DE Human MrgX3 (mas-related gene) protein.
XX KW Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
XX KW receptor; sensory perception; pain; analgesic; MrgX3.
XX OS Homo sapiens.
XX PN WO200183555-A2.
XX PD 08-NOV-2001.
XX PF 04-MAY-2001; 2001WO-US014519.
XX PR 04-MAY-2000; 2000US-0202027P.
XX PR 01-AUG-2000; 2000US-0222344P.
XX PR 03-NOV-2000; 2000US-00704707.
XX PR 19-APR-2001; 2001US-0285493P.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Anderson DJ, Dong X, Zylka M, Han S, Simon M;
XX WPI; 2002-171346/22.
XX DR N-PSDB; AAD33751.

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XX Isolated polypeptide, Mr_g, which is a G-protein coupled receptor and an
PT isolated polypeptide, drg-12, which is also a receptor, useful for
PT identifying agonists or antagonists for treating pain.
XX
XX Claim 16; Page 130; 185pp; English.

XX The invention relates to Mr_g (mas-related gene) protein, which is a G-
CC protein coupled receptor and drg-12 protein, which is a receptor. The
CC invention is useful for identifying compounds that bind to it, especially
CC agonists or antagonists. Administration of an agent (e.g. the identified
CC agonist) that increases the expression of Mr_g in a mammal may be used for
CC treating impaired sensory perception in a mammal, especially pain. The
CC antagonist may also be useful for treating impaired sensory perception in
CC a mammal. The present sequence is human Mr_gX3 protein

XX Sequence 322 AA;

Query Match 100.0%; Score 1688; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRVRNA 60
DB |||||
1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRVRNA 60

QY 61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120
DB |||||
61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120

QY 121 CLSILWPIWHCRPRYLSSVMCVLLWALSILSLLEWPCDFLFGADSVWCETSDFIT 180
DB |||||
121 CLSILWPIWHCRPRYLSSVMCVLLWALSILSLLEWPCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSLVLLVRLCGSRKMPLETLVTLTLLVFLLCGLPFGIOWALFS 240
DB |||||
181 IAWLVFLCVLGGSLVLLVRLCGSRKMPLETLVTLTLLVFLLCGLPFGIOWALFS 240

QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300
DB |||||
241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322

DB |||||
301 VDEGGWLPQETLELSGRLEQ 322

RESULT 4

ID ABP81750 standard; protein; 322 AA.

AC ABP81750;

DT 04-MAR-2003 (first entry)

DE Human G protein-coupled receptor Mr_gX3 protein SEQ ID NO:674.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

OS OS

FN WO200261087-A2.

XX

PD 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42595.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR) useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample, or
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX Sequence 322 AA;

Query Match 100.0%; Score 1688; DB 6; Length 322;

Best Local Similarity 100.0%; Pred. No. 2e-174;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRVRNA 60
DB |||||
1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRVRNA 60

QY 61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120
DB |||||
61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120

QY 121 CLSILWPIWHCRPRYLSSVMCVLLWALSILSLLEWPCDFLFGADSVWCETSDFIT 180
DB |||||
121 CLSILWPIWHCRPRYLSSVMCVLLWALSILSLLEWPCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSLVLLVRLCGSRKMPLETLVTLTLLVFLLCGLPFGIOWALFS 240
DB |||||
181 IAWLVFLCVLGGSLVLLVRLCGSRKMPLETLVTLTLLVFLLCGLPFGIOWALFS 240

QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300
DB |||||
241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322

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Db          301 VDEGGGWLFPQETLELSGRLEQ 322
|||||
RESULT 5
AAU97598
ID AAU97598 standard; protein; 337 AA.
XX AC
XX AAU97598;
XX DT
XX 12-AUG-2002 (first entry)
XX DE
XX Human G-protein coupled receptor (GPCR).
XX
XX Human; G-protein coupled; receptor; GPCR; human protease;
XX human therapeutic protein; query sequence; search; chromosome 3;
XX sequence database; non-human transgenic animal; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 41..61
FT /label= Helix_1
FT Domain 75..95
FT /label= Helix_2
FT Domain 112..132
FT /label= Helix_3
FT Modified-site 133..135
FT /note= Protein kinase C (PKC) phosphorylation site"
FT Domain 151..171
FT /label= Helix_4
FT Modified-site 169..172
FT /note= "Casein kinase II (CK2) phosphorylation site"
FT Modified-site 181..184
FT /note= "Casein kinase II (CK2) phosphorylation site"
FT Domain 193..213
FT /label= Helix_5
FT Modified-site 221..223
FT /note= "Protein kinase C (PKC) phosphorylation site"
FT Domain 229..249
FT /label= Helix_6
FT Modified-site 244..249
FT /note= "Myristoylation site"
FT Modified-site 248..253
FT /note= "Myristoylation site"
FT Domain 261..281
FT /label= Helix_7
FT Modified-site 279..282
FT /note= "Asn glycosylation site"
FT Modified-site 292..294
FT /note= "Protein kinase C (PKC) phosphorylation site"
FT Modified-site 333..336
FT /note= "Casein kinase II (CK2) phosphorylation site"
XX
XX WO200234914-A1.
XX
XX 02-MAY-2002.
XX
XX 10-OCT-2001; 2001WO-US031592.
XX
XX 25-OCT-2000; 2000US-00695045.
XX
XX 31-MAY-2001; 2001US-00867570.
XX
XX (PEKE ) PE CORP NY.
XX
XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;
XX WPI; 2002-463360/49.
XX
XX N-PSDB; ABK52822, ABK52823.
XX
XX Novel isolated G-protein coupled receptor peptide useful for treating
XX disorder characterized by absence of, in appropriate or unwanted
XX expression of the receptor protein, and as immunogens to raise

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PT antibodies.
XX Claim 1; Fig 2; 75pp; English.
XX
XX The present invention relates to a new G-protein coupled receptor (GPCR)
XX peptide. The invention is useful for identifying a modulator of GPCR and
XX for treating a disease or condition mediated by a human protease. The
XX invention is also useful as models for the development of human
XX therapeutics, for identifying therapeutic proteins, as targets for
XX development of human therapeutic agents, and as query sequence to perform
XX a search against sequence databases to, for e.g., identify other family
XX members of related sequences. The vector of the invention is useful for
XX producing a GPCR protein or peptide, for conducting cell-based assays
XX involving a GPCR protein or its fragment, for identifying GPCR protein
XX mutants whose functions are affected, and to produce non-human transgenic
XX animals. The present amino acid sequence represents the human G-protein
XX coupled receptor (GPCR) protein of the invention. This sequence is
XX encoded by the human G-protein coupled receptor (GPCR) gene located on
XX chromosome 3
XX
XX Sequence 337 AA;
XX
XX Query Match 100.0%; Score 1688; DB 5; Length 337;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-174;
XX Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MDSTIPVLGTETLTINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
XX Db 16 MDSTIPVLGTETLTINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 75
XX
XX QY 61 VSIYILNVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
XX Db 76 VSIYILNVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
XX
XX QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLSILEWMECDFLFGADSVWCETSDFIT 180
XX Db 136 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLSILEWMECDFLFGADSVWCETSDFIT 195
XX
XX QY 181 IAWLVFLCVLGGSSLLVRLVILCGSRKNPLTRLYVTILTVLVLGCLPFGIOWALFS 240
XX Db 196 IAWLVFLCVLGGSSLLVRLVILCGSRKNPLTRLYVTILTVLVLGCLPFGIOWALFS 255
XX
XX QY 241 RIHLDWKVLVCHVHLVSIIFLSALNSSANPIIYFVGSFRQRNQRNKLVLQALQDTPE 300
XX Db 256 RIHLDWKVLVCHVHLVSIIFLSALNSSANPIIYFVGSFRQRNQRNKLVLQALQDTPE 315
XX
XX QY 301 VDEGGGWLFPQETLELSGRLEQ 322
XX Db 316 VDEGGGWLFPQETLELSGRLEQ 337
XX
XX RESULT 6
XX AAU970762
XX ID AAU970762 standard; protein; 322 AA.
XX
XX AC AAU970762;
XX
XX 18-AUG-2000 (first entry)
XX
XX Human G protein-coupled receptor hHI7T213V SEQ ID NO.2.
XX
XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
XX genetic disease; cellular function regulation.
XX
XX Homo sapiens.
XX
XX WO200020455-A1.
XX
XX 13-APR-2000.
XX
XX 30-SEP-1999; 98WO-JP005366.
XX
XX 01-OCT-1998; 98JP-00279535.

```


XX (TAKE) TAKEDA CHEM IND LTD.
 XX PA Watanabe T, Terao Y, Matsui H;
 XX PI
 XX PF
 XX DR WPI; 2000-303747/26.
 XX DR N-PSDB; AAA29812.
 XX
 XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
 XX PT e.g. in determining ligands and treatment of diseases associated with
 XX PT dysfunction of the protein.
 XX
 XX Claim 2; Page 92-93; 97pp; Japanese.
 XX
 XX The present sequence represents a human-derived G protein-coupled protein
 XX CC designated hH7T213V, which is isolated from the human hippocampus. The G
 XX CC protein-coupled receptor can be used for preventing, treating and
 XX CC diagnosing genetic diseases associated with G protein-coupled protein,
 XX CC and for regulating cellular functions. The protein can be used to prevent
 XX CC and treat disorders associated with G protein-coupled protein gene
 XX CC dysfunction. It can also be used to identify G protein-coupled protein
 XX CC ligands and generating antibodies and antisera against the protein. It is
 XX CC also useful in constructing recombinant receptor protein expressing
 XX CC systems, developing receptor-binding assay systems and screening drug
 XX CC candidates, and can be used as a probe in the genetic diagnosis of G
 XX CC protein-coupled protein disorders
 XX
 XX Sequence 322 AA;
 SQ

Query Match 99.7%; Score 1683; DB 3; Length 322;
 Best Local Similarity 99.7%; Pred. No. 6.8e-174;
 Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 DB 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 QY 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSVMCVLLWALSRLSILEWFCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSVMCVLLWALSRLSILEWFCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLRYVTILLTVLVFLLCGLPFGIQWALFS 240
 DB 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLRYVTILLTVLVFLLCGLPFGIQWALFS 240
 QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 DB 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 QY 301 VDEGGGWLPOETLELSGRLEQ 322
 DB 301 VDEGGGWLPOETLELSGRLEQ 322

RESULT 7
 ADC86821
 ID ADC86821 standard; protein; 322 AA.
 XX
 XX AC ADC86821;
 XX
 XX DT 01-JAN-2004 (first entry)
 XX
 XX DE Human GPCR protein SEQ ID NO:1274.
 XX
 XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 XX gene therapy.
 XX OS Homo sapiens.
 XX

PN EF1270724-A2.
 XX
 XX PD 02-JAN-2003.
 XX
 XX PF 18-JUN-2002; 2002EP-00013517.
 XX
 XX PR 18-JUN-2001; 2001JP-00246789.
 XX
 XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX
 XX PF; 2003-315783/31.
 XX DR N-PSDB; ADC86820.
 XX
 XX New polynucleotide, useful for preparing a composition for treating a
 XX PT patient in need of increased or suppressed activity or expression of the
 XX PT guanosine triphosphate-binding protein coupled receptor.
 XX
 XX Claim 2; SEQ ID NO 1274; 28pp; English.
 XX
 XX The invention relates to a novel polynucleotide encoding a guanosine
 XX CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 XX CC the invention may have a use in gene therapy. The polynucleotide and
 XX CC polypeptide are useful for preparing a composition for treating a patient
 XX CC in need of increased or suppressed activity or expression of the
 XX CC guanosine triphosphate-binding protein coupled receptor. The protein
 XX CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
 XX
 XX Sequence 322 AA;
 SQ

Query Match 99.7%; Score 1683; DB 7; Length 322;
 Best Local Similarity 99.7%; Pred. No. 6.8e-174;
 Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 DB 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 QY 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSVMCVLLWALSRLSILEWFCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSVMCVLLWALSRLSILEWFCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLRYVTILLTVLVFLLCGLPFGIQWALFS 240
 DB 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLRYVTILLTVLVFLLCGLPFGIQWALFS 240
 QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 DB 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 QY 301 VDEGGGWLPOETLELSGRLEQ 322
 DB 301 VDEGGGWLPOETLELSGRLEQ 322

RESULT 8
 AAB14846
 ID AAB14846 standard; protein; 322 AA.
 XX
 XX AC AAB14846;
 XX
 XX DT 19-DEC-2000 (first entry)
 XX
 XX DE Human novel G-protein coupled receptor #1.
 XX
 XX KW Human; novel G-protein coupled receptor; signal transduction;
 XX disease diagnosis; drug screening; disease therapy.
 XX

XX OS Homo sapiens.
 XX XX WO2000040724-A1.
 XX PD 13-JUL-2000.
 XX XX 04-JAN-2000; 2000WO-US0000052.
 XX XX 04-JAN-1999; 99US-0114566P.
 XX PR 14-JAN-1999; 99US-0115828P.
 XX XX (LEXI-) LEXICON GENETICS INC.
 XX XX Nehls M, Wattler F;
 XX PI WPI; 2000-465986/40.
 XX DR N-PSDB; AAA70342.
 XX XX New polynucleotides encoding novel G-protein coupled receptors useful for
 PT diagnosis, drug screening, clinical trial monitoring and for the
 PT treatment of physiological or behavioral disorders.
 XX PS Claim 1; Page 53-54; 61pp; English.
 XX XX The present sequence is the protein sequence for a novel human G-protein
 CC coupled receptor (NGPCR). These proteins are involved in signal
 CC transduction pathways in many cases. The protein contains seven
 CC transmembrane domains, and is expressed in human testis, mammary gland
 CC and salivary gland tissue. The protein, its gene, agonists, antagonists
 CC and antibodies can be used to diagnose and treat diseases associated with
 CC the inappropriate expression or expression of mutant versions of the
 CC protein, for screening for drugs which can be used in the same manner,
 CC and for elucidating the function of the protein.
 XX XX Sequence 322 AA;

Query Match 98.5%; Score 1663; DB 3; Length 322;
 Best Local Similarity 99.4%; Pred. No. 1e-171;
 Matches 320; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTIPNGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCMRRA 60
 DB 1 MDSTIPVLGTELTIPNGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCMRRA 60
 QY 61 VSIYILNLVAADFLSGHIICSPRLNINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLSGHIICSPRLNINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVLGGSSLVLLVRLICGSRKMPITRLVVTILLTVLVFLLCGLPFGIOWALFS 240
 DB 181 IAWLVFLCVLGGSSLVLLVRLICGSRKMPITRLVVTILLTVLVFLLCGLPFGIOWALFS 240
 QY 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTPE 300
 DB 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTPE 300
 QY 301 VDEGGWLPQETLELSGSRLEQ 322
 DB 301 VDEGGWLPQETLELSGSRLEQ 322

RESULT 9

AAV30159

ID AAY20159 standard; protein; 322 AA.

XX AC AAY30159;

XX DT 20-MAR-2003 (revised)

DT 26-NOV-1999 (first entry)
 XX Human dorsal root receptor 1 hDRR1.
 XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
 KW hDRR1; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
 XX Homo sapiens.
 XX WO9932519-A1.
 XX PD 01-JUL-1999.
 XX PF 16-DEC-1998; 98WO-SE002348.
 XX PR 22-DEC-1997; 97SE-00004836.
 XX XX (ASTR) ASTRA PHARMA INC.
 XX PA (ASTR) ASTRA AB.
 XX XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
 XX WPI; 1999-405162/34.
 XX DR N-PSDB; AAZ10067.
 XX XX Rat and human dorsal root receptors and related polynucleotides, useful
 PT for identifying agents for anesthesia and analgesia.
 XX PS Claim 6; Page 39-41; 72pp; English.
 XX XX This is the human dorsal root receptor 1 (hDRR1) protein sequence. This
 CC is a G protein coupled receptor that is expressed preferentially in
 CC dorsal root ganglia. hDRR1 can be used to create antibodies against
 CC hDRR1. The dorsal root ganglia area of the central nervous system (CNS)
 CC is densely innervated with primary or afferent neurons involved in
 CC transmission, modulation and sensation of pain. The DR's which are
 CC expressed in this region of the CNS may be used for assays for the
 CC identification of new agents for anaesthesia and analgesia. (Updated on
 CC 20-MAR-2003 to correct PA field.)
 XX XX Sequence 322 AA;

Query Match 97.3%; Score 1642; DB 2; Length 322;
 Best Local Similarity 97.2%; Pred. No. 1.9e-169;
 Matches 313; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTIPNGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCMRRA 60
 DB 1 MDSTIPVLGTELTIPNGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCMRRA 60
 QY 61 VSIYILNLVAADFLSGHIICSPRLNINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLSGHIICSPRLNINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVLGGSSLVLLVRLICGSRKMPITRLVVTILLTVLVFLLCGLPFGIOWALFS 240
 DB 181 IAWLVFLCVLGGSSLVLLVRLICGSRKMPITRLVVTILLTVLVFLLCGLPFGIOWALFS 240
 QY 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTPE 300
 DB 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTPE 300
 QY 301 VDEGGWLPQETLELSGSRLEQ 322
 DB 301 VDEGGWLPQETLELSGSRLEQ 322

RESULT 10

AAV30160

DB 301 VDEGGWMLPQETLELSGSKLE 321

RESULT 11
ABP96695
ID ABP96695 standard; protein; 302 AA.
XX
AC ABP96695;
XX
DT 03-JUN-2003 (first entry)
XX
DE Human G protein-coupled receptor DRG7 protein SEQ ID NO:10.
XX
KW Human; G protein-coupled receptor; GPCR; DRG; pain; sensory transduction.
XX
OS Homo sapiens.
XX
PN WO2003023010-A2.
XX
PD 20-MAR-2003.
XX
PF 06-SEP-2002; 2002WO-US028619.
XX
PR 07-SEP-2001; 2001US-0317879P.
XX
PA (IRMI-) IRM LLC.
XX
PI Liao J, Gray NS, Caldwell JC, Schultz PG;
XX
DR WPI; 2003-301064/29.
XX
DR N-PSDB; ACC44771.
XX
PT Novel G-protein coupled receptor polypeptide expressed in mammalian
XX sensory neurons of dorsal root ganglia, useful as target for screening
XX for agents that regulate pain.
XX
PS Claim 10; Page 50; 51pp; English.
XX
CC The present invention describes human G protein-coupled receptor (GPCR)
XX proteins (I) designated DRG1, DRG2, DRG4, DRG6, DRG7, and DRG8 (see
XX ABP96691 to ABP96695) encoded by ACC44767 to ACC44772. (I) can be used
XX for identifying a compound that modulates pain, by contacting a compound
XX with (I), and selecting a compound that binds to the extracellular domain
XX of that modulates GPCR activity of the polypeptide. Such compounds that
XX modulate the activity of (I) can be used to investigate the role of (I)
XX in sensory (e.g. pain) transduction. Biologically active (I) can be used
XX for testing inhibitors and activators of (I) as pain transducers or pain
XX inhibitors using in vivo and in vitro expression that measure e.g.
XX transcriptional activation of (I), ligand binding, phosphorylation and
XX dephosphorylation, binding to G-proteins, G-protein activation,
XX regulatory molecule binding, voltage, membrane potential and conductance
XX changes, ion flux, intracellular second messengers such as cAMP and
XX inositol triphosphate, intracellular calcium levels and neurotransmitter
XX release. Such activators and inhibitors identified using (I) can be used
XX to further study sensory transduction and to identify specific pain
XX agonists and antagonists. The modulators can be administered directly to
XX the mammalian subject for modulation of pain in vivo

Query Match 92.2%; Score 1557; DB 6; Length 302;
Best Local Similarity 93.5%; Pred. No. 3e-160;
Matches 301; Conservative 1; Mismatches 0; Indels 20; Gaps 1;
Sequence 302 AA;

QY 1 MDSTIPVLGTETLPINGREETPCYKQLSTFTGTCIVSLVALTGNVAVLLGCRMRNA 60
DB 1 MDSTIPVLGTETLPINGREETPCYKQLSTFTGTCIVSLVALTGNVAVLLGCRMRNA 40
QY 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
DB 41 VSIYILNLVAADFLSLGHIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 100
QY 121 CLSILWPIWYHCRPRYLSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180

AAAY30160 standard; protein; 322 AA.
AAAY30160;
20-MAR-2003 (revised)
26-NOV-1999 (first entry)
Human dorsal root receptor 2 hDRR2.
Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
hDRR2; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
Homo sapiens.
WO9932519-A1.
01-JUL-1999.
16-DEC-1998; 98WO-SE002348.
22-DEC-1997; 97SE-00004836.
(ASTR) ASTRA PHARMA INC.
(ASTR) ASTRA AB.
Ahmad S, Barville D, Fortin Y, Lembo P, O'donnell D, Shen S;
WPI; 1999-405162/34.
N-PSDB; AAZ10068.
Rat and human dorsal root receptors and related polynucleotides, useful
for identifying agents for anaesthesia and analgesia.
Claim 11; Page 43-45; 72pp; English.
This is the human dorsal root receptor 2 (hDRR2) protein sequence. This
is a G protein coupled receptor that is expressed preferentially in
dorsal root ganglia. hDRR2 can be used to create antibodies against
hDRR2. The dorsal root ganglia area of the central nervous system (CNS)
is densely innervated with primary or afferent neurons involved in
transmission, modulation and sensation of pain. The DR's which are
expressed in this region of the CNS may be used for assays for the
identification of new agents for anaesthesia and analgesia. (Updated on
20-MAR-2003 to correct PA field.)
Sequence 322 AA;

Query Match 94.7%; Score 1598; DB 2; Length 322;
Best Local Similarity 95.6%; Pred. No. 1.2e-164;
Matches 307; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTETLPINGREETPCYKQLSTFTGTCIVSLVALTGNVAVLLGCRMRNA 60
DB 1 MDSTIPVLGTETLPINGREETPCYKQLSTFTGTCIVSLVALTGNVAVLLGCRMRNA 60
QY 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWYHCRPRYLSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVLCVVGSSILVLRILCGSRKMPRLRYVITLLTVLVFLLCGLPFGIQWALFS 240
DB 181 IAWLVLRVLCGSSILVLRILCGSRKMPRLRYVITLLTVLVFLLCGLPFGIQWALFS 240
QY 241 RHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKVLQRLQDTPE 300
DB 241 RHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNLKVLQRLQDTPE 300
QY 301 VDEGGWMLPQETLELSGSKLE 321

Db 101 CUSILPWIYHCRPRYLSSVMCVLLWALSLSRILEWMFCDFLFGANSVWCETSDFIT 160
QY 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 240
Db 161 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 220
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQLKVLQALQDTPE 300
Db 221 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQLKVLQALQDTPE 280
QY 301 VDEGGWLPQETLELSGSRLQ 322
Db 281 VDEGGWLPQETLELSGSRLQ 302

RESULT 12
AA30161
ID RAY30161 standard; protein; 322 AA.
XX
AC AA30161;
XX
XX
DT 20-MAR-2003 (revised)
DT 26-NOV-1999 (first entry)
XX
DE Human dorsal root receptor 3 hDRR3.
XX
KW Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
KW hDRR3; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
XX
CS Homo sapiens.
XX
XX WO9932519-A1.
XX
XX 01-JUL-1999.
XX
XX 16-DEC-1998; 98WO-SE002348.
XX
XX 22-DEC-1997; 97SE-00004836.
XX
XX (ASTR) ASTRA PHARMA INC.
XX (ASTR) ASTRA AB.
XX
XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
XX
XX WPI; 1999-405162/34.
XX N-PSDB; AAZ10069.
XX
XX Rat and human dorsal root receptors and related polynucleotides, useful
XX for identifying agents for anesthesia and analgesia.
XX
XX Claim 16; Page 48-50; 72pp; English.

This is the human dorsal root receptor 3 (hDRR3) protein sequence. This
is a G protein coupled receptor that is expressed preferentially in
dorsal root ganglia. hDRR3 can be used to create antibodies against
hDRR3. The dorsal root ganglia area of the central nervous system (CNS)
is densely innervated with primary or afferent neurons involved in
transmission, modulation and sensation of pain. The DRG's which are
expressed in this region of the CNS may be used for assays for the
identification of new agents for anaesthesia and analgesia. (Updated on
20-MAR-2003 to correct PA field.)

Sequence 322 AA;
Query Match 83.2%; Score 1405; DB 2; Length 322;
Best Local Similarity 83.9%; Pred. No. 1e-143;
Matches 270; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGRETFPCYKQLSFTGLCTIVSLVALTGNVAVMLLGRMRNA 60
Db 1 MDPTVSLDTELTLPINGTEETLCYKQLSLVLCIVSLVGLTGNVAVMLLGRMRNA 60

QY 61 VSIYILNLVAADFLSLGHIICSPRLNIRHRFISKILSPVMTFPYFGLSMLSAISTER 120
Db 61 FSIYILNLAAADFLSLGRIIYLLSFISPHITISKILYPMVFSYFAGLNFLSAVSTDR 120
QY 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLSRILEWMFCDFLFGADSVCWCTSDFIT 180
Db 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLSRILEWMFCDFLFGADSVCWCTSDFIT 180
QY 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 240
Db 181 VAWIIFLCVLCGSSLVLLVRLICGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQLKVLQALQDTPE 300
Db 241 WIHVDREVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGSRLQ 322
Db 301 VDEGGWLPQETLELSGSRLQ 322

RESULT 13
ADCL2766
ID ADCL2766 standard; protein; 304 AA.
XX
AC ADCL2766;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human GPCR protein, SEQ ID NO 98.
XX
KW G protein-coupled receptor; GPCR; antibacterial; fungicide; protozoacide;
KW virucide; antirheumatic; antiarthritic; tranquiliser; antidiabetic;
KW osteopathic; neurotropic; neuroprotective; anorectic; cardiac;
KW neuroleptic; cystostatic; antiparkinsonian; hypotensive; hypertensive;
KW antiulcer; antiallergic; anticonvulsant; analgesic; infection;
KW rheumatoid arthritis; chronic obstructive pulmonary diseases; COPD;
KW asthma; non-insulin dependent diabetes; obesity; osteoporosis;
KW Alzheimer's disease; age-related macular degeneration;
KW myocardial infarction; schizophrenia; osteoarthritis; cancer;
KW Parkinson's disease; congestive heart failure; hypotension; hypertension;
KW ulcer; allergy; benign prostatic hyperplasia; seizure disorder; anxiety;
KW obsessive compulsive disorder; Cushing's syndrome; hypopituitarism; pain;
human.
XX
XX Homo sapiens.
XX
XX WO2003000893-A2.
XX
XX 03-JAN-2003.
XX
XX 24-JUN-2002; 2002WO-IB002357.
XX
XX 26-JUN-2001; 2001US-0301095P.
XX 06-NOV-2001; 2001US-0333185P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Martinez RMA, Sigurdsson GT;
XX WPI; 2003-210155/20.
XX N-PSDB; ADCL2765.
XX
XX New G protein-coupled receptor (GPCR) genes and polypeptides, useful for
PT diagnosing diseases associated with a GPCR, or in gene therapy for
PT treating e.g. obesity, osteoporosis, Alzheimer's, cancers or congestive
PT heart failure.
XX
XX Claim 10; SEQ ID NO 98; 253pp; English.
XX
XX The invention relates to a novel isolated nucleic acid of a G protein-
CC coupled receptor (GPCR) gene comprising any of 62 sequences of 312-2454
CC bp, or its complements; a GPCR polypeptide comprising any of 62 sequences

of 291-818 amino acids; or a nucleic acid that hybridises, under high stringency conditions, with any of the 62 GPCR sequences or any of their complements. The GPCR agents of the invention have the following activities: antibacterial, fungicide, protozoacide, virucide, antirheumatic, tranquiliser, antiarthritic, antidiabetic, osteopathic, neurotropic, neuroprotective, anorectic, cardiant, neuroleptic, cytostatic, antiparkinsonian, hypotensive, hypertensive, antiulcer, antiallergic, anticonvulsant, and analgesic. The GPCR therapeutic agent, particularly a GPCR gene agonist or antagonist, is useful for treating a disease or condition associated with a GPCR in an individual. The nucleic acid cited above, which is 100 or fewer nucleotides in length, is useful for assaying a sample for the presence of the GPCR gene nucleic acid or a GPCR gene nucleic acid with at least one nucleotide difference from a first nucleic acid, or for diagnosing a susceptibility to a disease or conditions associated with a GPCR. These diseases include infections (e.g. bacterial, fungal, protozoan or viral), rheumatoid arthritis, chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, obesity, osteoporosis, Alzheimer's disease, age-related macular degeneration, myocardial infarction, schizophrenia, osteoarthritis, cancers, Parkinson's diseases, congestive heart failure, hypertension, hypotension, ulcers, allergies, benign prostatic hyperplasia, seizure disorder, anxiety, obsessive compulsive disorder, Cushing's syndrome, hypopituitarism, or pain. This sequence represents one of the 62 GPCR proteins of the invention.

XX Sequence 304 AA;

Query Match 82.9%; Score 1399; DB 7; Length 304;

Best Local Similarity 99.6%; Pred. No. 4.3e-143;

Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 CYKQLSFTGLTCIYSLVALTGNVAVLMLGCMRRNAVSIYILNLVAADFLLSGHIC 82
DB 1 CYKQLSFTGLTCIYSLVALTGNVAVLMLGCMRRNAVSIYILNLVAADFLLSGHIC 60
QY 83 SPLRLINRHPIKSLSPVMTPTFYIGLSMLSAISTERCLSIPLWYCHRRPRLSSVM 142
DB 61 SPLRLINRHPIKSLSPVMTPTFYIGLSMLSAISTERCLSIPLWYCHRRPRLSSVM 120
QY 143 CYYLWALSLSRLSILEMFCDFLPSGADSVWCETSDFTIAMLVLCVVLGSSLLVLR 202
DB 121 CYYLWALSLSRLSILEMFCDFLPSGADSVWCETSDFTIAMLVLCVVLGSSLLVLR 180
QY 203 LCGSRKMPLTRLYVILLTVLVFLLCGLPFGIQWALFRIHLDKWLKVLCHVLSIFLSA 262
DB 181 LCGSRKMPLTRLYVILLTVLVFLLCGLPFGIQWALFRIHLDKWLKVLCHVLSIFLSA 240
QY 263 LNSSANPIIYFFVGSFRQRQNLKL 289
DB 241 LNSSANPIIYFFVGSFRQRQNLKL 267

RESULT 14

AY30162

ID AAY30162 standard; protein; 322 AA.

XX AC AAY30162;

XX DT 20-MAR-2003 (revised)

DT 26-NOV-1999 (first entry)

XX DE Human dorsal root receptor 4 hDRR4.

XX KW Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;

KW hDRR4; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Misc-difference 310 /note= "Encoded by GAC"

FT Misc-difference 312 /note= "Encoded by ATC"

FT

XX WO9932519-A1.

XX PD 01-JUL-1999.

XX PF 16-DEC-1998; 98WO-SE002348.

XX PR 22-DEC-1997; 97SE-00004836.

XX PA (ASTR) ASTRA PHARMA INC.

XX PA (ASTR) ASTRA AB.

XX PI Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;

XX WPI; 1999-405162/34.

XX DR N-PSDB; AAZ10070.

XX PT Rat and human dorsal root receptors and related polynucleotides, useful

PT for identifying agents for anaesthesia and analgesia.

XX PS Claim 21; Page 52-54; 72pp; English.

XX CC This is the human dorsal root receptor 4 (hDRR4) protein sequence. This

CC is a G protein coupled receptor that is expressed preferentially in

CC dorsal root ganglia. hDRR4 can be used to create antibodies against

CC hDRR4. The dorsal root ganglia area of the central nervous system (CNS)

CC is densely innervated with primary or afferent neurons involved in

CC transmission, modulation and sensation of pain. The DRR's which are

CC expressed in this region of the CNS may be used for assays for the

CC identification of new agents for anaesthesia and analgesia. (Updated on

CC 20-MAR-2003 to correct PA field.)

XX SQ Sequence 322 AA;

Query Match 82.4%; Score 1391; DB 2; Length 322;

Best Local Similarity 83.9%; Pred. No. 3.4e-142;

Matches 270; Conservative 16; Mismatches 36; Indels 0; Gaps 0;

QY 1 MDSFTIPVLGTELPINGREBETPCYKQTLSTGLTCTIVSLVALTGNVAVLMLGCMRRNA 60
DB 1 MDSFTVSLDTELPINGTEETLCYKQTLSTGLTCTIVSLVALTGNVAVLMLGCMRRNA 60
QY 61 VSIYILNLVAADFLLSGHICSPBLINIRHPIKSLSPVMTPTFYIGLSMLSAISTER 120
DB 61 FSIYILNLVAADFLLSGHILYSLSPISPHITISKILYPMWMSYFAGLSFLSAVSTER 120
QY 121 CLSLTLPWYCHRRPRLSSVMCVLLWALSLSRLSILEMFCDFLPSGADSVWCETSDFIT 180
DB 121 CLSLVLPWYCHRRPRLSSVMCVLLWALSLSRLSILEMFCDFLPSGADSVWCETSDFIT 180
QY 181 IAWLVLCVVLGSSLLVLRILCGSRKMPLTRLYVILLTVLVFLLCGLPFGIQWALFS 240
DB 181 VAWLVLCVVLGSSLLVLRILCGSRKMPLTRLYVILLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLDKWLKVLCHVLSIFLSALNSSANPIIYFFVGSFRQRQNLKLVLQALQDTP 300
DB 241 WIHVDREVLFCHVLSIFLSALNSSANPIIYFFVGSFRQRQNLKLVLQALQDASE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 15

AY87664

ID AAY87664 standard; protein; 322 AA.

XX AC AAY87664;

XX DT 11-AUG-2000 (first entry)

XX DE Human G protein-coupled receptor protein #2.

XX

KW G protein-coupled receptor protein; human; treatment; diagnosis;
XX genetic disorder.

XX Homo sapiens.

XX WO200020456-A1.

XX 13-APR-2000.

XX 30-SEP-1999; 99WO-JF005365.

XX 01-OCT-1998; 98JP-00279512.

XX 20-OCT-1998; 98JP-00298667.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Watanabe T, Terao Y, Fukusumi S;

XX WPI; 2000-303748/26.

XX N-PSDB; AAA12208.

XX Novel human-originated G protein-coupled protein and encoding nucleic
PT acid useful for e.g. identifying ligands and treating diseases
PT associated with dysfunction of the protein.

XX Claim 2; Page 97-98; 105pp; Japanese.

XX This invention describes a novel human G protein-coupled receptor protein
CC (1). The products of the invention can be used for preventing, treating
CC and diagnosing gene diseases and for regulating cellular functions. The
CC protein can be used to identify ligands and generate antibodies and
CC antisera. It is also useful in the construction of a recombinant receptor
CC protein expression system, developing a receptor-binding assay system and
CC screening drug candidates and as a probe in diagnosing genetic disorders
CC involving G protein-coupled protein. This sequence represents a human G-
CC protein coupled receptor protein described in the method of the invention
XX

SQ Sequence 322 AA;

Query Match 82.2%; Score 1387; DB 3; Length 322;
Best Local Similarity 84.1%; Pred. No. 9.4e-142;
Matches 269; Conservative 20; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDSIPVLGTELTPINGREETPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCRMRNA 60
DB 1 MDPTVPVLGKLTIPINGREETPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLFLSGHIIFCSPLRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
DB 61 VSIYILNLAAADFLFLSFQIIRSPRLINISHLIRKILSVMTFPYFGLSMLSAISTER 120

QY 121 CLSILMPITWHCRPRVLSVWCVLLNALSLRSLRILEWMPFCDLFGADSVWCETSDFIT 180
DB 121 CLSVLMPITWYRCRPTHLUSAVCVLLWGLSLFLSNLEWRFCDFLFGADSSWCETSDFI 180

QY 181 IAWLFLCVLSCGSSLVLLVRLICGSRMPITRLVYTLITLVFLVLLCGLPFGIOWALFS 240
DB 181 VAWLFLCVLSCVSSLVLLVRLICGSRMPITRLVYTLITLVFLVLLCGLPFGILGALIY 240

QY 241 RIHLDKVLFCHVHLVSTFLSALNSSANPIIYFVFGSFRQFQFQFQFQFQFQFQFQFQ 300
DB 241 RMHLNLEVLVCHVILVCMVLSLSSANPIIYFVFGSFRQFQFQFQFQFQFQFQFQFQ 300

QY 301 VDEGGGWLPOETLELSGRL 320
DB 301 VDXGEGQLPEESLELSGRL 320

Search completed: July 4, 2004, 08:43:45
Job time : 78 secs

NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-52

Query Match 23.0%; Score 388.5; DB 1; Length 282;
Best Local Similarity 34.4%; Pred. No. 7.2e-27;
Matches 96; Conservative 53; Mismatches 87; Indels 43; Gaps 7;

QY 37 VSLVALTGNVAVLW-----LLGCRMRNAVSIYIINL-VAADFLFLSG 78
Db 9 ISPGVFVENGILLWFLCFFVYTHLSADIISLFC-----IFILSDIADLYELSSG 60
QY 79 HIICSPRLNIRHPISKILSPVMTFFYIGLSMISAISTERCLSIWPIWYCHRRPYL 138
Db 61 H-----YTVITLSVTELFYNTGLYLLTAISVERCLSVLYP-WYRCHRPKYQ 108
QY 139 SSMCVILWALSILRSILEWFCDFLFGADSVWCETSDFTITAWLVFLCVLGGSSLV 198
Db 109 SALVCALLWALSCLVTM-YMCDIRFEESHNRDCRAVIFIALSPLVFTSPVSTIL 167
QY 199 LVRILCGSRKMPRLXVITLLTVLVFLCGLPFGIQWALFSRIHLDWKVLFCHVLSI 258
Db 168 VVKIRKNTWASHSSKLYIVIMVTIIFLIPAMPRLLYLYEY---WST-FGNLHHISL 223
QY 259 FLSALNSANPIIYFFVGSFRQRQNLKVLQALQD 297
Db 224 LFTSTINSANPIIYFFVGSFKKFKESLKVLTAFKQD 262

RESULT 3
PCT-US93-08528-52
Sequence 52, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-52

Query Match 23.0%; Score 388.5; DB 5; Length 282;
Best Local Similarity 34.4%; Pred. No. 7.2e-27;
Matches 96; Conservative 53; Mismatches 87; Indels 43; Gaps 7;

QY 37 VSLVALTGNVAVLW-----LLGCRMRNAVSIYIINL-VAADFLFLSG 78
Db 9 ISPGVFVENGILLWFLCFFVYTHLSADIISLFC-----IFILSDIADLYELSSG 60
QY 79 HIICSPRLNIRHPISKILSPVMTFFYIGLSMISAISTERCLSIWPIWYCHRRPYL 138
Db 61 H-----YTVITLSVTELFYNTGLYLLTAISVERCLSVLYP-WYRCHRPKYQ 108
QY 139 SSMCVILWALSILRSILEWFCDFLFGADSVWCETSDFTITAWLVFLCVLGGSSLV 198
Db 109 SALVCALLWALSCLVTM-YMCDIRFEESHNRDCRAVIFIALSPLVFTSPVSTIL 167
QY 199 LVRILCGSRKMPRLXVITLLTVLVFLCGLPFGIQWALFSRIHLDWKVLFCHVLSI 258
Db 168 VVKIRKNTWASHSSKLYIVIMVTIIFLIPAMPRLLYLYEY---WST-FGNLHHISL 223
QY 259 FLSALNSANPIIYFFVGSFRQRQNLKVLQALQD 297
Db 224 LFTSTINSANPIIYFFVGSFKKFKESLKVLTAFKQD 262

RESULT 4
US-08-118-270-76
Sequence 76, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004


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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-76

Query Match      20.4%; Score 344; DB 1; Length 298;
Best Local Similarity 31.3%; Pred. No. 6.6e-23;
Matches 94; Conservative 58; Mismatches 114; Indels 34; Gaps 11;

QY 33 LTCIVSLVALTGNAVLLGCRMRNAVSIYI--LNLVAADFLFLSGHICSPRLINI 90
DB 8 LLCLCGLV--GNGVLVWFFGFSIKRTPFSIYVFLHIASADGIYLFSAV---IALLNM 61
QY 91 RHPISKI-----LSPVMTFPYFGLSMLSAISTERCLSIILPWIWCHRRPYLSSVMCV 144
DB 62 GTFLGSPDPYVRVRSRIVGLTFFAGVSLLPALSIERCVSIFPMWYRRRPKRLSAGVCA 121
QY 145 LLWALSILRLSEWFCDFLFGADSVWCETSDFTIIAWLF-----LCVVLGSSSLVLL 199
DB 122 LLWLSFLVTSIHNYFC--LLGHEASGTACLNMDISLGLLFFLFCPIWVLPFC---IAL 176
QY 200 VRILGSRKMLPT--RLYVTILLTVLVLGCLPFGIOWALFSRIHLDW--KVLFCVHLV 256
DB 177 LHVECRARRQRSAXLNHVLAIVSVFLVSSYILGIDWFLF-----WVFQIPAPPEYV 230
QY 257 SIFLSALNSSANPIIYFVGSFRQRNQLKVLQALQDTPVEDEGGWLPQ--TLEL 315
DB 231 RLCLICINSSAKPIVITFAGRDKSQRLWBLRVVFORALRDGAEPGDAASPTNTVTNEM 290

RESULT 5
PCT-US93-08528-76
Sequence 76, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NETMARK
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-76

Query Match      20.4%; Score 344; DB 5; Length 298;
Best Local Similarity 31.3%; Pred. No. 6.6e-23;
Matches 94; Conservative 58; Mismatches 114; Indels 34; Gaps 11;

QY 33 LTCIVSLVALTGNAVLLGCRMRNAVSIYI--LNLVAADFLFLSGHICSPRLINI 90
DB 8 LLCLCGLV--GNGVLVWFFGFSIKRTPFSIYVFLHIASADGIYLFSAV---IALLNM 61
QY 91 RHPISKI-----LSPVMTFPYFGLSMLSAISTERCLSIILPWIWCHRRPYLSSVMCV 144
DB 62 GTFLGSPDPYVRVRSRIVGLTFFAGVSLLPALSIERCVSIFPMWYRRRPKRLSAGVCA 121
QY 145 LLWALSILRLSEWFCDFLFGADSVWCETSDFTIIAWLF-----LCVVLGSSSLVLL 199
DB 122 LLWLSFLVTSIHNYFC--LLGHEASGTACLNMDISLGLLFFLFCPIWVLPFC---IAL 176
QY 200 VRILGSRKMLPT--RLYVTILLTVLVLGCLPFGIOWALFSRIHLDW--KVLFCVHLV 256
DB 177 LHVECRARRQRSAXLNHVLAIVSVFLVSSYILGIDWFLF-----WVFQIPAPPEYV 230
QY 257 SIFLSALNSSANPIIYFVGSFRQRNQLKVLQALQDTPVEDEGGWLPQ--TLEL 315
DB 231 RLCLICINSSAKPIVITFAGRDKSQRLWBLRVVFORALRDGAEPGDAASPTNTVTNEM 290

RESULT 6
US-08-981-825-6
Sequence 6, Application US/08981825
Patent No. 6040426
GENERAL INFORMATION:
APPLICANT: OGAWA, KAZUYAUKI
APPLICANT: TANAKA, KINUYA
APPLICANT: NAGATA, KINYA
APPLICANT: TAKANO, SYOICHI
TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe, Martens, Olson & Bear
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
```

```

; APPLICATION NUMBER: US/08/981,825
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: MSHIM4.001APC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-825-6

Query Match 15.1%; Score 255.5; DB 3; Length 395;
Best Local Similarity 25.9%; Pred. No. 6.2e-15;
Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;

QY 36 IVSLVLTGNVAVLWLLGCMRRNAVSIYILNLVAADFL-----FLS-----G 78
DB 41 LASLGLGVNGVILFVVGCRMQTQVTTVWLHLASDLASASLPFFTYFLAVGHSWELG 100
QY 79 HIICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTERCLSLIWPYHCHREPRYL 138
DB 101 TTFC-----KLHSSIFFLNMFASGFLLSAISLDRCLQVVRPVAQNHTVAA 147
QY 139 SSVMCVLLWALSRLSILEMFCDFLPSGADSVWC-----E 174
DB 148 AHKVCVLWALAVLNTVYFVFRDTISRLDGRIMCYNVLLNPGDPDRDATCNSRQAALA 207
QY 175 TSDPTITAWLFLCVLVCSSLVLLVRLCGSRKMPLTRLYVTILLTVLVLGCPFGI 234
DB 208 VSKPL-LAFVLPLAIASSHAASVSL-RLQHRGRRP-GRFVRLVAAVVAALCWGPYHV 264
QY 235 QWALFSPRIH-----LDWKVLFCHVHLVSIFLSAL---NSSANPIIYFFVGSFRQQR 284
DB 265 FSLLEARAHANPGLRPLVWRGL-----PFVTSIAFFNSVANPVLVLTCPDMLRKL 316
QY 285 QNLKVLQALQDTPEVDEGG 305
DB 317 RSLRTVLESVLVDSDSELGGAG 337

RESULT 7
US-09-480-784-6
; Sequence 6, Application US/09480784
; Patent No. 6166186
; GENERAL INFORMATION:
; APPLICANT: OGAWA, KAZUYAUKI
; TANAKA, KAZUYA
; NAGATA, KINYA
; TAKANO, SYOICHI
; TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; APPLICATION NUMBER: US/08/981,825
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: MSHIM4.001APC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-825-6

Query Match 15.1%; Score 255.5; DB 3; Length 395;
Best Local Similarity 25.9%; Pred. No. 6.2e-15;
Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;

QY 36 IVSLVLTGNVAVLWLLGCMRRNAVSIYILNLVAADFL-----FLS-----G 78
DB 41 LASLGLGVNGVILFVVGCRMQTQVTTVWLHLASDLASASLPFFTYFLAVGHSWELG 100
QY 79 HIICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTERCLSLIWPYHCHREPRYL 138
DB 101 TTFC-----KLHSSIFFLNMFASGFLLSAISLDRCLQVVRPVAQNHTVAA 147
QY 139 SSVMCVLLWALSRLSILEMFCDFLPSGADSVWC-----E 174
DB 148 AHKVCVLWALAVLNTVYFVFRDTISRLDGRIMCYNVLLNPGDPDRDATCNSRQAALA 207
QY 175 TSDPTITAWLFLCVLVCSSLVLLVRLCGSRKMPLTRLYVTILLTVLVLGCPFGI 234
DB 208 VSKPL-LAFVLPLAIASSHAASVSL-RLQHRGRRP-GRFVRLVAAVVAALCWGPYHV 264
QY 235 QWALFSPRIH-----LDWKVLFCHVHLVSIFLSAL---NSSANPIIYFFVGSFRQQR 284
DB 265 FSLLEARAHANPGLRPLVWRGL-----PFVTSIAFFNSVANPVLVLTCPDMLRKL 316
QY 285 QNLKVLQALQDTPEVDEGG 305
DB 317 RSLRTVLESVLVDSDSELGGAG 337

RESULT 8
US-07-759-568-2
; Sequence 2, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-2

Query Match 14.0%; Score 235.5; DB 1; Length 354;
Best Local Similarity 28.9%; Pred. No. 3.2e-13;
Matches 94; Conservative 53; Mismatches 12; Indels 57; Gaps 16;
QY 10 TELTPINGRETEPC--YKQTLS--FTGLTCTVSVALTGNA--VVLWLLGCRMRNAVSI 63
DB 23 TQMPVE-KDYSFCLVVTQNLKVVVYVIALVLLSLGSLWMLVLYSRNSRVTDV 81
QY 64 YILNLVAADFLLSGHICSP--RLNIRHPISKILSPVMTFFYIGLSMLSAISTERC 121
DB 82 YLLNLAMAP-APCPDHVGLRQGRKLDFTPLCKVSLVKEVNFYSGILLACTISVDY 140
QY 122 LSILNPIWHCHRRPYLSSVMCVLWALSILERSILEWMFCDFLPGADSVNC-ETSDFIT 180
DB 141 LAIVST-RTLTQKRLVKFICGLWALSILSLPFFLRQVFSNNSPVCYEDLGHNT 199
QY 181 IAWLVLCVVL-----CGSSVLVLRILC-GSRKXPLRLYV-----TILLVLVF 225
DB 200 AKW-----CWVLRLPHTFGFILPLVLMFLCYGFTLTLFOAHMGQKHRAMVIFAVLIF 255
QY 226 ILCGPFG-----IQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIY 272
DB 256 LLCWLPYNLVLLADTLMTHTVLTQTCQRNELDRALDATEI-----LGLHSLCLNPIY 309
QY 273 FVGSFRQQRQNRN--LKLVLQAL 295
DB 310 AFIG-----QNFENGFLKMLAARGL 329

RESULT 9
US-07-759-568-1
Sequence 1, Application US/07759568
Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-1

Query Match 13.4%; Score 226.5; DB 1; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;
QY 19 EETPCYKQTLSTFTG-----LTCIVSLVALTGNA--VVLWLLGCRMRNAVSIYILNLVAAD 72
DB 30 DAAPCEPESLEINKYFVWIYVIALVLLSLGSLWMLVLYSRVGSVTDVLLNLALAD 89
QY 73 FLF-----LSGHICSPRLNIRHPISKILSPVMTFFYIGLSMLSAIS 117
DB 90 LLFALPLIWAASKVNGWIFGFLC-----KVSLKEVNFYSGILLACIS 136
QY 118 TERCLSLNPIWYHCHRR---PRYLSVMCVLWALSILERSILEWMFCDFLPGADSVNC 173
DB 137 VDRYLAIV-----HATRTLTQKRLVKFICLSIWGLSLLALLFVLLFRRTVYSSNVSPAC 191
QY 174 -ETSDITTAWLVLVLCV--LCGSSVLVLRILC-GSRKXPLRLYV-----TILLT 221
DB 192 YEDMGNNTANWMLRLILPQSPGFIVPLLMFLCYGFTLTLFOAHMGQKHRAMVIFAV 251
QY 222 VLVLCLCGPFG-----IQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSAN 268
DB 252 VLFLLCWLPYNLVLLADTLMTHTVLTQTCQRNELDRALDATEI-----LGLHSLCLN 305
QY 269 PIYFFVG-SFR 279
DB 306 PLIYAFIGQKFR 317

RESULT 10
US-08-450-393A-8
Sequence 8, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-450-393A-8

Query Match 13.4%; Score 226.5; DB 1; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYQTLSTFTG-----LTCIVSLVALTGNA-VVLLGCGMRNNAVSIYILNLVAAD 72
DB 30 DAAPCEPESLEINKYFVVIIVALLVLLSLGSLVMLVILYSRVGRSVTDVYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAIS 117
DB 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSLKEVNFYSGILLACIS 136
QY 118 TERCLSLPIWVHCR-----PRYLSSVMCVLLWALSILSLRSLLEWMPDFLFGADSVWC 173
DB 137 VDRYLAIV-----HATRTLQKRYLVKFCISLWGLSLLALLPVLLFRRTVYSSNVSPAC 191
QY 174 -ETSDFITIAWLFLCV--LCGSSLVLLVRILC-GSRKMPLTRLYV-----TILLT 221
DB 192 YEDMGNTANRWMLRLIPQSGFIVPLLMFCYGTLTFLFAHMGQKRAMRVIFAV 251
QY 222 VLVLICGLPFG-----IQWALFSRIHLDKVLFCVHLVLSIFLSALNSSAN 268
DB 252 VLIFLLCWLPYNVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSLCN 305
QY 269 PIYFFVVG-SFR 279
DB 306 PLIYAFIGQKFR 317

RESULT 11
US-08-390-000A-5
Sequence 5, Application US/08390000A
Patent No. 5985583
GENERAL INFORMATION:
APPLICANT: Sealton, Stuart C.
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,000A
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6923-052
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-390-000A-5

Query Match 13.4%; Score 226.5; DB 2; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYQTLSTFTG-----LTCIVSLVALTGNA-VVLLGCGMRNNAVSIYILNLVAAD 72
DB 30 DAAPCEPESLEINKYFVVIIVALLVLLSLGSLVMLVILYSRVGRSVTDVYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAIS 117
DB 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSLKEVNFYSGILLACIS 136
QY 118 TERCLSLPIWVHCR-----PRYLSSVMCVLLWALSILSLRSLLEWMPDFLFGADSVWC 173
DB 137 VDRYLAIV-----HATRTLQKRYLVKFCISLWGLSLLALLPVLLFRRTVYSSNVSPAC 191
QY 174 -ETSDFITIAWLFLCV--LCGSSLVLLVRILC-GSRKMPLTRLYV-----TILLT 221
DB 192 YEDMGNTANRWMLRLIPQSGFIVPLLMFCYGTLTFLFAHMGQKRAMRVIFAV 251
QY 222 VLVLICGLPFG-----IQWALFSRIHLDKVLFCVHLVLSIFLSALNSSAN 268
DB 252 VLIFLLCWLPYNVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSLCN 305
QY 269 PIYFFVVG-SFR 279
DB 306 PLIYAFIGQKFR 317

RESULT 12
US-08-446-669-8
Sequence 8, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669

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; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELE: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PCT-US95-00476-8

Query Match      13.4%; Score 226.5; DB 3; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYKQTLSTG-----LTCIVSLVLTGNA-VVLMILGCRMRNNAVSIYILNLVAAD 72
Db 30 DAAPCEPESLEINKYFVWIYIALVFLSLGNSLWLVILYSRQSVTDVYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLNIRHPISKILSPVMTFFPYFGLSMLSAIS 117
Db 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSSLKEVNFYSGILLACIS 136
QY 118 TERCLSIIMPWYHCR-----PRYLSSVMCVLLWALSILRSILEWMFCDFLFGSADSVWC 173
Db 137 VDRYLAIV-----HATRTLTKQKYLKFKICLSINGLSLLALPVLFRRTVSSNVSPAC 191
QY 174 -ETSDFTITAWLVFLCVV--LCGSSILVLLVRILC-GSRKMPLTRLV-----TILLT 221
Db 192 YEDMGNNTANWMLRLIPQSGFIVPLLMFCYGTFLRTLKFAHMGQKHRAWRVIFAV 251
QY 222 VLVLFLCGLPFG-----IQWALFSRIHLDKVKVLFCHVHLVSIFLSALNSSAN 268
Db 252 VLIFLLCWLPLYNVLLADTLMTQVQTCERNHIDRALDATEI-----LGILHSCLN 305
QY 269 PIYFFVVG-SFR 279
Db 306 PLIYAFIGQKFR 317

RESULT 13
PCT-US95-00476-8
; Sequence 8, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELE:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PCT-US95-00476-8

Query Match      13.4%; Score 226.5; DB 5; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYKQTLSTG-----LTCIVSLVLTGNA-VVLMILGCRMRNNAVSIYILNLVAAD 72
Db 30 DAAPCEPESLEINKYFVWIYIALVFLSLGNSLWLVILYSRQSVTDVYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLNIRHPISKILSPVMTFFPYFGLSMLSAIS 117
Db 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSSLKEVNFYSGILLACIS 136
QY 118 TERCLSIIMPWYHCR-----PRYLSSVMCVLLWALSILRSILEWMFCDFLFGSADSVWC 173
Db 137 VDRYLAIV-----HATRTLTKQKYLKFKICLSINGLSLLALPVLFRRTVSSNVSPAC 191
QY 174 -ETSDFTITAWLVFLCVV--LCGSSILVLLVRILC-GSRKMPLTRLV-----TILLT 221
Db 192 YEDMGNNTANWMLRLIPQSGFIVPLLMFCYGTFLRTLKFAHMGQKHRAWRVIFAV 251
QY 222 VLVLFLCGLPFG-----IQWALFSRIHLDKVKVLFCHVHLVSIFLSALNSSAN 268
Db 252 VLIFLLCWLPLYNVLLADTLMTQVQTCERNHIDRALDATEI-----LGILHSCLN 305
QY 269 PIYFFVVG-SFR 279
Db 306 PLIYAFIGQKFR 317

RESULT 14
US-08-202-056-7
; Sequence 7, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 70693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-202-056-7

Query Match
13.4%; Score 226.5; DB 1; Length 360;
Best Local Similarity 26.3%; Pred. No. 2.1e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYKQTLSTFG-----LTCIVSLVALTGNA-VVLWLLGCRMRNAVSIYILNLVAAD 72
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 35 DAAPCEPESLEINKYFVVIIVLVALLGSLVILVSVGRSVTDVILLNLALAD 94
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAIS 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 95 LLFALTLPWAASKVNGWIFGTFLC-----KVVSLLKEVNFYSGILLACIS 141
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QY 118 TERCLSILWPIWYHCR-----PRYLSSVMCVLLWALSLSLSILEWMFCDFLPSGADSVWC 173
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Db 142 VDRYLAIV-----HATRTLQKRYLVKVFICLSINGLSLLALPVLLFRRTVYSSNVSPAC 196
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QY 174 -ETSDFITIAWLVLGVV--LCGSSLVLLVRLC-GSRKMPLTRLV-----TILTT 221
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 YEDMGNTANWRMLLRILPQSGFIVPLLMFCYGTTLTLFKAHMGQKRAMRVIFAV 256
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 VLVELLCGLPFG-----IQWALFSRIHLDKVLFCFHVHLVSIFLSALNSSAN 268
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 VLIFELCWLPYNLVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSCLN 310
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 269 PIIVFFVG-SFR 279
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 311 PLIVAFIQKXFR 322
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Job time : 25 secs

; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 70693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-202-056-7

Query Match
13.4%; Score 226.5; DB 1; Length 360;
Best Local Similarity 26.3%; Pred. No. 2.1e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYKQTLSTFG-----LTCIVSLVALTGNA-VVLWLLGCRMRNAVSIYILNLVAAD 72
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 35 DAAPCEPESLEINKYFVVIIVLVALLGSLVILVSVGRSVTDVILLNLALAD 94
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAIS 117
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 95 LLFALTLPWAASKVNGWIFGTFLC-----KVVSLLKEVNFYSGILLACIS 141
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 TERCLSILWPIWYHCR-----PRYLSSVMCVLLWALSLSLSILEWMFCDFLPSGADSVWC 173
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 VDRYLAIV-----HATRTLQKRYLVKVFICLSINGLSLLALPVLLFRRTVYSSNVSPAC 196
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 -ETSDFITIAWLVLGVV--LCGSSLVLLVRLC-GSRKMPLTRLV-----TILTT 221
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 YEDMGNTANWRMLLRILPQSGFIVPLLMFCYGTTLTLFKAHMGQKRAMRVIFAV 256
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 VLVELLCGLPFG-----IQWALFSRIHLDKVLFCFHVHLVSIFLSALNSSAN 268
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 VLIFELCWLPYNLVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSCLN 310
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 269 PIIVFFVG-SFR 279
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 311 PLIVAFIQKXFR 322
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-409-778-4
; Sequence 4, Application US/09409778
; Patent No. 6472173
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: A NOVEL CHEMOKINE RECEPTOR OBTAINED FROM
; TITLE OF INVENTION: A CDNA LIBRARY OF FETAL LIVER-SPLEEN
; FILE REFERENCE: 20411-742CON2 (now 28110/360578)
; CURRENT APPLICATION NUMBER: US/09/409,778
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/12829
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/236,166
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: US 09/106,800
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-409-778-4

Query Match
13.4%; Score 226.5; DB 4; Length 360;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:45:34 ; Search time 79 Seconds
(without alignments)
1268.777 Million cell updates/sec

Title: US-09-787-879C-1

Perfect score: 1688

Sequence: 1 MDSIPVLGTELTPINGREE.....EGGWLQFQTELSGSRLEQ 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1688	100.0	322	10	US-09-995-225-20
3	1688	100.0	322	12	US-10-072-012-529
4	1688	100.0	322	12	US-10-072-012-534
5	1688	100.0	322	14	US-10-183-116-31
6	1688	100.0	322	14	US-10-225-567A-674
7	1688	100.0	322	12	US-09-867-570-2
8	1683	99.7	322	12	US-10-072-012-530
9	1683	99.7	322	12	US-10-072-012-535
10	1683	99.7	322	12	US-10-401-397A-2
11	1683	99.7	322	15	US-10-292-798-1274
12	1683	98.5	322	12	US-10-391-074-2
13	1683	97.1	314	14	US-10-219-834-79
14	1557	92.2	302	14	US-10-237-467-10
15	1383	81.9	322	12	US-10-016-248-81

Sequence 172, App
Sequence 527, App
Sequence 533, App
Sequence 44, Appl
Sequence 16, Appl
Sequence 4, Appl
Sequence 1056, Ap
Sequence 4, Appl
Sequence 20, Appl
Sequence 12, Appl
Sequence 898, App
Sequence 528, App
Sequence 532, App
Sequence 18, Appl
Sequence 84, Appl
Sequence 531, App
Sequence 536, App
Sequence 33, Appl
Sequence 669, App
Sequence 4, Appl
Sequence 174, App
Sequence 1042, Ap
Sequence 178, App
Sequence 20, Appl
Sequence 12, Appl
Sequence 24, Appl
Sequence 4, Appl
Sequence 16, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-995-225-20
; Sequence 20, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pridge, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208

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; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-20

Query Match      100.0%; Score 1688; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLLSGHICSPRLINIRHPISKILSPVMTFPFYIGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLLSGHICSPRLINIRHPISKILSPVMTFPFYIGLSMLSAISTER 120
QY 121 CLSILPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLPGADSVWCETSDFIT 180
Db 121 CLSILPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLPGADSVWCETSDFIT 180
QY 181 IAWLFLCVVLCGSSLLVLRILCGSKMPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
Db 181 IAWLFLCVVLCGSSLLVLRILCGSKMPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDMKVLFCFVHLVSIIFLSALNSSANPIIYFVGSFRQRNRQNLKVLQALQDTPE 300
Db 241 RIHLDMKVLFCFVHLVSIIFLSALNSSANPIIYFVGSFRQRNRQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 2
US-09-995-225-20
; Sequence 20, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human C
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
```

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; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-20

Query Match      100.0%; Score 1688; DB 10; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLLSGHICSPRLINIRHPISKILSPVMTFPFYIGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLLSGHICSPRLINIRHPISKILSPVMTFPFYIGLSMLSAISTER 120
QY 121 CLSILPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLPGADSVWCETSDFIT 180
Db 121 CLSILPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLPGADSVWCETSDFIT 180
QY 181 IAWLFLCVVLCGSSLLVLRILCGSKMPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
Db 181 IAWLFLCVVLCGSSLLVLRILCGSKMPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDMKVLFCFVHLVSIIFLSALNSSANPIIYFVGSFRQRNRQNLKVLQALQDTPE 300
Db 241 RIHLDMKVLFCFVHLVSIIFLSALNSSANPIIYFVGSFRQRNRQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 3
US-10-072-012-529
; Sequence 529, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
```



```
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 529
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-529

Query Match      100.0%; Score 1688; DB 12; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTELTPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSLSILEWFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSLSILEWFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCGSSSLVLLVRLICGSRKMPPLRLVYVITLLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSSLVLLVRLICGSRKMPPLRLVYVITLLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGSLEQ 322
Db 301 VDEGGWLPQETLELSGSLEQ 322

RESULT 4
US-10-072-012-534
/ Sequence 534, Application US/10072012
/ Publication No. US20040033493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zerhusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Li, Li
```

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/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier, Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgees, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 534
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-534

Query Match      100.0%; Score 1688; DB 12; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTELTPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSLSILEWFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSLSILEWFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCGSSSLVLLVRLICGSRKMPPLRLVYVITLLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSSLVLLVRLICGSRKMPPLRLVYVITLLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
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QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 5
US-10-183-116-31
; Sequence 31, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 05/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-31

Query Match 100.0%; Score 1688; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTPLTPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDSTIPVLGTPLTPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120

QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPFGIQWALFS 240

QY 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSRQRQRNQLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSRQRQRNQLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 7
US-09-867-570-2
; Sequence 2, Application US/09867570
; Publication No. US20040076951A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/695,045
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-867-570-2

Query Match 100.0%; Score 1688; DB 12; Length 337;
Best Local Similarity 100.0%; Pred. No. 5e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTPLTPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDSTIPVLGTPLTPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120

QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPFGIQWALFS 240

QY 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSRQRQRNQLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSRQRQRNQLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 6
US-10-225-567A-67A
; Sequence 67A, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
```

Db 16 MDSTIPVLGTETLPINGREETPCYKOTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 75
Qy 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 76 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
Qy 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 136 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 195
Qy 181 IAWLVFLCVLGGSLVLLVRLILGSRKMPRLTRLYVTILLTVLVLGGLPFGIOWALFS 240
Db 196 IAWLVFLCVLGGSLVLLVRLILGSRKMPRLTRLYVTILLTVLVLGGLPFGIOWALFS 255
Qy 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKLVLRALQDTPE 300
Db 256 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKLVLRALQDTPE 315
Qy 301 VDEGGWLPQETLELSGSRLEQ 322
Db 316 VDEGGWLPQETLELSGSRLEQ 337

RESULT 8

US-10-072-012-530
; Sequence 530, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 530
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-530

Query Match 99.7%; Score 1683; DB 12; Length 322;
Best Local Similarity 99.7%; Pred. NO. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSTIPVLGTETLPINGREETPCYKOTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTETLPINGREETPCYKOTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Qy 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Qy 181 IAWLVFLCVLGGSLVLLVRLILGSRKMPRLTRLYVTILLTVLVLGGLPFGIOWALFS 240
Db 181 IAWLVFLCVLGGSLVLLVRLILGSRKMPRLTRLYVTILLTVLVLGGLPFGIOWALFS 240
Qy 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKLVLRALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKLVLRALQDTPE 300
Qy 301 VDEGGWLPQETLELSGSRLEQ 322
Db 301 VDEGGWLPQETLELSGSRLEQ 322

RESULT 9

US-10-072-012-535
; Sequence 535, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31

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; PRIORITY APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 535
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-072-012-535

Query Match          99.7%; Score 1683; DB 12; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSILSLLEWFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSILSLLEWFCDFLFGADSVWCETSDFIT 180
QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSILSLLEWFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSILSLLEWFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLWDKVLFCVHLVSLIFLSALNSSANPIIYFVGSFRQRQRNKLVLQALQDTPE 300
Db 241 RIHLWDKVLFCVHLVSLIFLSALNSSANPIIYFVGSFRQRQRNKLVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 10
US-10-401-397A-2
; Sequence 2, Application US/10401397A
; Publication No. US20030212001A1
; GENERAL INFORMATION:
; APPLICANT: Perri, Krishna G.
; APPLICANT: Moffett, Daniel
; APPLICANT: Abran, Daniel
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION AND TREATMENT OF ELEVATED
; TITLE OF INVENTION: INTRAOCULAR PRESSURE AND RELATED CONDITIONS
; FILE REFERENCE: 4518/1M674US1
; CURRENT APPLICATION NUMBER: US/10/401,397A
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/367,513
; PRIOR FILING DATE: 2002-03-27
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-401-397A-2

Query Match          99.7%; Score 1683; DB 12; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSILSLLEWFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSILSLLEWFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLWDKVLFCVHLVSLIFLSALNSSANPIIYFVGSFRQRQRNKLVLQALQDTPE 300
Db 241 RIHLWDKVLFCVHLVSLIFLSALNSSANPIIYFVGSFRQRQRNKLVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 11
US-10-292-798-1274
; Sequence 1274, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1274
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-798-1274

Query Match          99.7%; Score 1683; DB 15; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
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QY 121 CUSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
Db 121 CUSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCSSSVLVAIRILCGSRKMPRLRYVYVITLLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVVLCSSSVLVAIRILCGSRKMPRLRYVYVITLLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 12
US-10-391-074-2
; Sequence 2, Application US/10391074
; Publication No. US20040038345A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael
; APPLICANT: Wattler, Frank
; TITLE OF INVENTION: No. US20040038345A1e1 Human Seven-Transmembrane Receptors
; FILE REFERENCE: 7705 0008-00-000
; CURRENT FILING DATE: US/10/391,074
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-391-074-2

Query Match 98.5%; Score 1663; DB 12; Length 322;
Best Local Similarity 99.4%; Pred. No. 1e-146;
Matches 320; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTLPINGRETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGRETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
QY 121 CUSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
Db 121 CUSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCSSSVLVAIRILCGSRKMPRLRYVYVITLLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVVLCSSSVLVAIRILCGSRKMPRLRYVYVITLLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 13
US-10-219-834-79
; Sequence 79, Application US/10219834
; Publication No. US20030036751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE

FILE REFERENCE: D0191 NP
CURRENT APPLICATION NUMBER: US/10/219,834
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,858
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/340,703
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: US 60/318,675
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/355,596
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 60/333,417
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/338,367
PRIOR FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 192
SOFTWARE: Patent in version 3.1
SEQ ID NO 79
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-834-79

Query Match 97.1%; Score 1639; DB 14; Length 314;
Best Local Similarity 97.5%; Pred. No. 1.7e-144;
Matches 314; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 MDSTIPVLGTLPINGRETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGRETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
QY 121 CUSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
Db 121 CUSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCSSSVLVAIRILCGSRKMPRLRYVYVITLLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVVLCSSSVLVAIRILCGSRKMPRLRYVYVITLLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 293 VDEGGWLPQETLELSGRLEQ 314

RESULT 14
US-10-237-467-10
; Sequence 10, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Jiayu
; APPLICANT: Gray, Nathanael S.
; APPLICANT: Caldwell, Jeremy C.
; APPLICANT: Schultz, Peter G.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Sensory Neuron Receptors
; FILE REFERENCE: 021288-001300US
; CURRENT APPLICATION NUMBER: US/10/237,467
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/317,879
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 302
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
; OTHER INFORMATION: 7 (DRG7) (NT009307)
US-10-237-467-10

Query Match          92.2%; Score 1557; DB 14; Length 302;
Best Local Similarity 93.5%; Pred. No. 7-2e-137;
Matches 301; Conservative 1; Mismatches 0; Indels 20; Gaps 1;

QY 1 MDSTIPVLGTELTPIINGRETPCYKQTLSTGLTCTIVSLVLTGNAVVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTELTPIINGREE-----ALTGNAVVLWLLGCRMRNA 40

QY 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
DB 41 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 100

QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGSADSVWCETSDFIT 180
DB 121 CLSVLWPIWYHCRPHTLSAVVCVLLWALSILRSILEWMFCDFLFGSADSVWCETSDFIT 180

QY 181 IAWLVFLCVVLCGSSLVLLVRLICGSRKMPITRLIYVTILLTVLVFLLCGLPFGIOWALFS 240
DB 181 VAWLIFLCVWLCGSSLVLLRILCGSRKIPITRLIYVTILLTVLVFLLCGLPFGIOWALFS 240

QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNRQNLKVLQALQDTP 300
DB 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNRQNLKVLQALQDASE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGQLPEBIELELSGRLEQ 322
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Search completed: July 4, 2004, 08:51:42
Job time : 90 secs

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RESULT 15
US-10-016-248-81
; Sequence 81, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-81

Query Match          81.9%; Score 1383; DB 12; Length 322;
Best Local Similarity 83.5%; Pred. No. 1.3e-120;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGRETPCYKQTLSTGLTCTIVSLVLTGNAVVLWLLGCRMRNA 60
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:33:34 ; Search time 26 Seconds
(without alignments)
1191.295 Million cell updates/sec

Title: US-09-787-879c-1
Perfect score: 1688
Sequence: 1 MDSTIPVGLTLPINGREE.....EGGWLPQETLESGSRLEQ 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	27.3	378	2 A39485	transforming prote
2	446.5	26.5	324	1 TVRTAS	transforming prote
3	430.5	25.5	325	1 TVRTAS	transforming prote
4	428.5	25.4	324	2 S51001	transforming prote
5	371	22.0	343	2 A38639	G protein-coupled
6	240	14.2	355	2 UQ1231	interleukin-8 rece
7	238	14.1	353	2 C42009	FMLP-related rece
8	235.5	14.0	354	2 A23669	interleukin-8 rece
9	226.5	13.4	360	2 A53611	interleukin-8 rece
10	220	13.0	358	2 A53752	interleukin-8 rece
11	219.5	13.0	369	2 A45291	somatostatin rece
12	219.5	13.0	369	2 A47195	somatostatin rece
13	217	12.9	351	2 B42009	FMLP-related rece
14	214.5	12.7	346	2 S22448	somatostatin rece
15	210.5	12.5	388	2 JN0605	somatostatin rece
16	210	12.4	473	2 JCS835	anaphylatoxin C3a
17	209.5	12.4	363	2 I57940	somatostatin rece
18	209	12.4	356	2 A20986	interleukin-8 rece
19	206	12.2	369	2 JC2083	somatostatin rece
20	205.5	12.2	355	2 A55733	G protein-coupled
21	205.5	12.2	384	2 A47249	brain-specific som
22	205	12.1	333	2 I65989	G protein-coupled
23	203.5	12.1	380	2 S36143	kappa opioid rece
24	202.5	12.0	380	2 A48227	kappa opioid rece
25	201.5	11.9	380	2 A55259	kappa opioid rece
26	201	11.9	352	2 A46520	N-formyl peptide r
27	199.5	11.8	380	2 JC2434	kappa opioid rece
28	199	11.8	369	2 B41795	somatostatin rece
29	198.5	11.8	380	2 JC2338	kappa opioid rece

complement C5a ana
G protein-coupled
somatostatin recep
interleukin-8 rece
somatostatin recep
somatostatin recep
G protein-coupled
N-formyl peptide c
tachykinin recepto
MIP-1 alpha recept
complement C5a ana
G protein-coupled
somatostatin recep
somatostatin recep
somatostatin recep
G protein-coupled

30 196.5 11.6 350 1 A37963
31 196.5 11.6 371 2 JC5498
32 196 11.6 384 2 JC4629
33 194.5 11.5 350 2 A39445
34 194 11.5 363 2 I57955
35 194 11.5 364 2 JN0763
36 193.5 11.5 375 2 JC5069
37 193 11.4 364 2 A49542
38 193 11.4 504 2 A41783
39 188 11.1 359 2 I49341
40 187.5 11.1 352 1 S27357
41 187 11.1 340 2 JC7695
42 186 11.0 391 2 A41795
43 186 11.0 391 2 C41795
44 186 11.0 391 2 A35297
45 185.5 11.0 353 2 JC2492

ALIGNMENTS

RESULT 1

A39485
transforming protein (mrg) - human
C/Species: Homo sapiens (man)
C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C/Accession: A39485
R/Monnot, C.; Weber, V.; Stinnakre, J.; Bihoreau, C.; Teutsch, B.; Clauser, J.
Mol. Endocrinol. 5, 1477-1487, 1991
A/Title: Cloning and functional characterization of a novel mas-related gene, modulation
C/Reference number: A39485; MUID:92130997; PMID:1723144
A/Accession: A39485
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-378 <WON>
A/Cross-references: GB:S78653; NID:G244209; PIDN:AAB21255.1; PID:G244210
C/Superfamily: mas transforming protein
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.3%; Score 461; DB 2; Length 378;
Best Local Similarity 37.9%; Pred. No. 2.9e-31;
Matches 107; Conservative 56; Mismatches 81; Indels 38; Gaps 10;

Qy 36 IVSLVATGNVWLLGCMRRNAVSTIYLNVAADFLSLGHIICSLRLINIR---- 91
Db 84 LVSLCGVLLNGTVFLCCG-ATNPYMYVILHLVAADVIYL-----CCSAVGFLQVTLTY 138
Qy 92 HPI-----SKILSPWTPPEYFGLSMLSAISTERCLSLWPIWYHCRPRYLSSVMCV 144
Db 139 HGVVFFIPDFLALSP---FSPVCLLLVAISTERCVCLVFLWYRCHRPKYTSNVVCT 195
Qy 145 LLWALSLLRSILEMFMFCDFLFGSDVWCTSD---FTIANL--VFLCVLGCSSILVLL 199
Db 196 LINGLPPFCINIVKSLFTY-----WKHVACVIFLKLGLFHALSLWMCVSLTLL 247
Qy 200 VRILGSRKMLRLVYVITLLTVLVLGLCPFGIQWALFSRIHLDKVLFCHVLSVIF 259
Db 248 IRLCCSQQKATRVAVQISAPMELLWALPLSV-----APLITDFKPVTTSYLSLIF 302
Qy 260 LSAINSSANPIIYFFVGSFQRQRNQLKVLQALODTPEV 301
Db 303 L-IINSSANPIIYFFVGSFLRKLKESLRVILQALADKPEV 343

RESULT 2

TVRTAS
transforming protein mas - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C/Accession: A31816
R/Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988
A/Title: Characterization of the rat mas oncogene and its high-level expression in the

A:Reference number: A31816; MUID:88276953; PMID:2455902
A:Accession: A31816
A:Molecule type: mRNA
A:Residues: 1-324 <YOU>
A:CROSS-references: GB:J03823; NID:G205313; PIDN:AAA41573.1; PID:G205314
C:Genetics:
A:Gene: mas
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; transforming protein; transmembrane protein
F:31-47/Domain: transmembrane #status predicted <TM1>
F:72-86/Domain: transmembrane #status predicted <TM2>
F:149-165/Domain: transmembrane #status predicted <TM3>
F:185-204/Domain: transmembrane #status predicted <TM4>
F:225-243/Domain: transmembrane #status predicted <TM5>

Query Match 26.5%; Score 446.5; DB 1; Length 324;
Best Local Similarity 38.08; Pred. No. 4.1e-30;
Matches 108; Conservative 57; Mismatches 96; Indels 23; Gaps 9;

QY 37 VSLVALTGNNAVLLGCRMRNAVSIYILNLVAADFLFSGHICS-----PLRLINIR 91
Db 41 ISPLGFVENGILLWFLCFRMRNPFTVYITHLSADIADLFCIFILSDYALDYELSSGH 100

QY 92 HPISKILSPVMTFFYFGLSMLSAISTERCLSIWPIWYHCRPRYLSSVMCVLLWALS 151
Db 101 YTTIVTSLVTFELFGYNTGLYLLTAISVERCLSVLYPIWYCHRPKQSAFVCALLWALS 160

QY 152 LRSILEMFCDFLFGSADSWCETSD-----FITI-AMLVFLCVLCGSSVLVLRILC 204
Db 161 LVTMEYVMC--IDSGEES--HSQSDCRAVIIFAILSLFVFTPLMLV-SSTILVVKIRK 215

QY 205 GSRKMPITRLYVITLLVFLVLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALN 264
Db 216 NTWASHSSKLYIVIMVTIIFLIPAMPVRVLYLLYVEY---WST-FGNLHNSILFSTIN 271

QY 265 SSANPIIYFFVGSFRQRNQLKVLORALQD--TPEVDEGG 306
Db 272 SSANPIIYFFVGSKKRRESKLVLTAFKDMQRRQEGNG 315

RESULT 3
TVHUAS
transforming protein mas - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Jun-1999
C:Accession: A01375
R:Young, D.; Waechter, G.; Birchmeier, C.; Pasano, O.; Wigler, M.
Cell 45, 711-719, 1986
A:Title: Isolation and characterization of a new cellular oncogene encoding a protein with
A:Reference number: A01375; MUID:86218084; PMID:3708691
A:Accession: A01375
A:Molecule type: DNA
A:Residues: 1-325 <YOU>
A:CROSS-references: GB:MJ3150; NID:G187388; PIDN:AAA36199.1; PID:G307158
C:Genetics:
A:Gene: GDB:MAS1
A:CROSS-references: GDB:120166; OMIM:165180
A:Map position: 6q24-6q27
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming protein
F:31-61/Domain: transmembrane #status predicted <TM1>
F:66-97/Domain: transmembrane #status predicted <TM2>
F:103-135/Domain: transmembrane #status predicted <TM3>
F:150-172/Domain: transmembrane #status predicted <TM4>
F:186-214/Domain: transmembrane #status predicted <TM5>
F:225-250/Domain: transmembrane #status predicted <TM6>
F:258-286/Domain: transmembrane #status predicted <TM7>
F:5.16,22,272/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.5%; Score 430.5; DB 1; Length 325;
Best Local Similarity 37.9%; Pred. No. 9.1e-29;
Matches 103; Conservative 56; Mismatches 94; Indels 19; Gaps 8;

QY 37 VSLVALTGNNAVLLGCRMRNAVSIYILNLVAADFLFSGHICS-----PLRLINIR 91
Db 42 ISPLGFVENGILLWFLCFRMRNPFTVYITHLSADIADLFCIFILSDYALDYELSSGH 101

QY 92 HPISKILSPVMTFFYFGLSMLSAISTERCLSIWPIWYHCRPRYLSSVMCVLLWALS 151
Db 102 YTTIVTSLVTFELFGYNTGLYLLTAISVERCLSVLYPIWYCHRPKQSAFVCALLWALS 161

QY 152 LRSILEMFCDFLFGSADSWCETSD-----FITI-AMLVFLCVLCGSSVLVLRILC 205
Db 162 LVTMEYVMC--IDSGEES--HSQSDCRAVIIFAILSLFVFTPLMLV-SSTILVVKIRK 217

QY 206 SRKMPITRLYVITLLVFLVLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALN 265
Db 218 TWASHSSKLYIVIMVTIIFLIPAMPVRVLYLLYVEY---WST-FGNLHNSILFSTIN 273

QY 266 SANPIIYFFVGSFRQRNQLKVLORALQD 297
Db 274 SANPIIYFFVGSKKRRESKLVLTAFKDMQRRQEGNG 305

RESULT 4
S51001
transforming protein mas - mouse
N:Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor mas
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2001
C:Accession: S51001; I48647; S29619
R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FEBS Lett. 357, 27-32, 1995
A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral
A:Reference number: S51001; MUID:95094925; PMID:8001672
A:Accession: S51001
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-324 <MET>
A:CROSS-references: EMBL:X67735
R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FEBS Lett. 357, 27-32, 1995
A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral
A:Reference number: I48647; MUID:95094925; PMID:8001672
A:Accession: I48647
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-87,'I',89-324 <RES>
A:CROSS-references: EMBL:X67735; NID:953011; PIDN:CAA47964.1; PID:G53012
C:Genetics:
A:Gene: mas
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; proto-oncogene; transmembrane protein

Query Match 25.4%; Score 428.5; DB 2; Length 324;
Best Local Similarity 37.7%; Pred. No. 1.3e-28;
Matches 107; Conservative 56; Mismatches 98; Indels 23; Gaps 9;

QY 37 VSLVALTGNNAVLLGCRMRNAVSIYILNLVAADFLFSGHICS-----PLRLINIR 91
Db 41 ISPLGFVENGILLWFLCFRMRNPFTVYITHLSADIADLFCIFILSDYALDYELSSGH 100

QY 92 HPISKILSPVMTFFYFGLSMLSAISTERCLSIWPIWYHCRPRYLSSVMCVLLWALS 151
Db 101 YTTIVTSLVTFELFGYNTGLYLLTAISVERCLSVLYPIWYCHRPKQSAFVCALLWALS 160

QY 152 LRSILEMFCDFLFGSADSWCETSD-----FITI-AMLVFLCVLCGSSVLVLRILC 204
Db 161 LVTMEYVMC--IDSGEES--HSQSDCRAVIIFAILSLFVFTPLMLV-SSTILVVKIRK 215

QY 205 GSRKMPITRLYVITLLVFLVLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALN 264
Db 216 NTWASHSSKLYIVIMVTIIFLIPAMPVRVLYLLYVEY---WST-FGNLHNSILFSTIN 271

QY 265 SSANPIIYFFVGSFRQRNQLKVLORALQD--TPEVDEGG 306

Db 272 SSANPIYFFVGSKKKRFRRESIKVLTTRAFKDEMFRQEGNG 315

RESULT 5

A35639

G protein-coupled receptor RTA - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999

C:Accession: A35639

R:Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Marcus, D.R.; Lynch, K.

A:Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue di

A:Reference number: A35639; MUID:90222168; PMID:2109324

A:Accession: A35639

A:Molecule type: mRNA

A:Residues: 1-343 <ROS>

A:Cross-references: GB:M35297; NID:G206809; PIN:AAA42087.1; PID:G206810; GB:M32098

C:Superfamily: mas transforming protein

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.0%; Score 371; DB 2; Length 343;

Best Local Similarity 33.1%; Pred. No. 9,3e-24;

Matches 99, Conservative 58, Mismatches 110; Indels 32; Gaps 11;

Qy 33 LTCIVSLVATGNVAVLWLGCMRRNNAVIYILNLVAADFLSGHIICSPURLNIR- 91

Db 53 LLCLCGIV--GNGLVWFFGFSIKTPFSYIFLHASADGIYLFSAV---IALLNGT 106

Qy 92 -----HPISKILSPVMTFPYFICGLSMLSAISTERCLSIWLPIWYHCRRPYILSSVM 142

Db 107 FLGSFPDYVRVSRIVG-LCTF--FAGVSLIPALSIERCVSIVFPWYWRPRKLSAGV 163

Qy 143 CVLLWALSLILRSILEWNPFCDFLPSGADSVNCEWTSDFTTIAWLVP--LCVVLGGSSILVLV 200

Db 164 CALLWLLSFLVTSIHNYFCMFLGCEASGCTACLNMD-LSLGILLFFLFCPLMWLPLCALIL 222

Qy 201 RILCGSRKMLPT-RLVYITLLTVLVLICGLPGCIQWALFSRIHLDW--KVLFCVHLVS 257

Db 223 HVECARRRQRSSAKLHNHVLVAISVFLVSIVYIGLDWFLP-----WVFQIPAPFPEYVT 276

Qy 258 IFLSALNSSANPIYFFVGSRQRQNLKVLQRALQDTPPEVDEGGWLPQE-TLEL 315

Db 277 DLICICINSSAKPIVYFLAGRDKSORLMEPLRVVFORALRDGAPGDGAASSTPTVTWEM 335

RESULT 6

interleukin-8 receptor - rabbit

QJ1231

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: QJ1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VanderBos, T.; Price, V.; Lyman, S.; Gerard

A:Title: Molecular characterization of the interleukin-8 receptor.

A:Reference number: QJ1231; MUID:91378994; PMID:1898400

A:Accession: QJ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:G165438; PIDN:AAA31375.1; PID:G165439

R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A:Reference number: A46483; MUID:92148149; PMID:1737938

A:Accession: A46483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:G165440; PIDN:AAA31376.1; PID:G165441

A:Experimental source: neutrophils

A>Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIIP:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	14.2%;	Score	240;	DB	2;	Length	355;	
Best Local Similarity	27.4%;	Pred.	No. 9.3e-13;					
Matches	92;	Conservative	57;	Mismatches	109;	Indels	78; Gaps 17;	
Qy	10	TELTPTNGREETPC--YKQTL	---	FTGLTCIVSLV	ALTGNA--VVLMLL	GCGRMRNA	VS	63
Db	23	TGMPPE--KDYSCLV	VTQLNKVVV	VIYALVFL	LSLGNL	VMLVIL	YSRNS	81
Qy	64	YIINLVAA	DFL	SGHII	CSPL	LN-----	I	117
Db	82	YLLNLAA	MDLLF---	ALTWPI	AVASKE	GWIGFT	PLCKV	137
Qy	118	TERCL	SIL	MP	IWH	CHRR----	PRYLS	173
Db	138	VDRY	LAIV----	HAT	RTL	QKHL	VKFCIG	192
Qy	174	-ETSD	FT	IIA	W	FL	CVV--	221
Db	193	YED	LGH	N	TAK	W	MLR	252
Qy	222	VLV	FL	CG	L	PG	FI	261
Db	253	VL	FL	CL	W	LYN	-----	299
Qy	262	AL	NS	AN	P	I	Y	295
Db	300	FL	AS	C	N	P	I	330

RESULT 7
C42009
FMLP-related receptor 2 - human
N:Alternate names: FMLP-related
receptor I; probable chemotactic receptor F2RH2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: C42009
R:Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A:Reference number: A42009: MURD:92307681: PMID:1612600

A:Residues: 1-353 <BAO>
A:Cross-references: GDS:W76673; NID:g182668; PID:g182659
C:Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears n
C:Genetics:
A:Gene: GDB:FPRL2
A:Cross-references: GDB:i128855; OMIM:136539
A:Map position: 19q13.3-19q13.4
A:Introns: #status absent
A:Protein family: vertebrate rhodopsin
C:Superfamily: vertebrate rhodopsin
C:Keywords: Chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match	14.1%	Score 238	DB 2	Length 353	
Best Local Similarity	23.8%	Pred. No. 1.4e-13			
Matches 81	Conservative 76	Mismatches 112	Indels 72	Gaps 15	
QY	14	PINGREE-----TPCYKQTLSTFTGLTCIVSLVALTGNAVLWLGLGCRVRRNAVSYYI	65		
DB	8	PLNETEEVLDEPAGHTVLWIFSLVHGVTFFVGL--GNGLVIWVAGERTVNTVITY	64		
QY	66	LNLVAADPLFLSGHIIICSPURLINI---RHP-----ISKILSPVMTPEPYFICGLSMLSAIS	117		
DB	65	LNLALAPFSFA---LTPFMVSVAMREKWPFFASFLCKLVHVMIDINLFSVVYLITIIA	120		
QY	118	TERCLSTLWPIWYICRPPRYLLSSVNCVLLWALSLLRSILEWMF-----CDPLP	165		
DB	121	LDRCICVLHFAQAQHRMTSLAKKWTGLMIFTVLTLPNPFIFWTITSTNGDTCYCIENP	180		
QY	166	SGADSVMWCET-----SDFTIAWLVFCVVLGCGSSLVLLVRLC-----G	205		

Db 181 ----AFWGDVAVLRNVFTMAKVFILHFIIGFTVPMSIITVCYGIITAAKHNRHMIKS 236
QY 206 SRKMPLTRLYVITLLVFLVLCGLPFP---GIQWALFSR---IHLDMKVLFCFVHLVSIF 259
Db 237 SR--PL-RVFAV---VASFFICWPFYELIGLIMAVLKEMLLNGKYKILVILNPIS-S 289
QY 260 LSAALNSANPIIYFFVGSFRQNRQNLKLVQLQALQDTPE 300
Db 290 LAFFNSCLNPILYVGMGRNFBRLIRSLPTSLSRALTEVPD 330
RESULT 8
A23669
interleukin-8 receptor, high affinity - rabbit
N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarero, J.
J: Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034; PMID:1700779
A:Accession: A23669
A:Molecule type: mRNA
A:Residues: 1-354 <THO>
A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil
Query Match 14.0%; Score 235.5; DB 2; Length 354;
Best Local Similarity 28.9%; Pred. No. 2.2e-12;
Matches 94; Conservative 53; Mismatches 121; Indels 57; Gaps 16;
QY 10 TELTPNGREETPC--YKOTLS---FTGLTCIVSLVALTGNA--VVLWLLGCRMRNAVSI 63
Db 23 TGNPPVE-KDYSCLVVTQTKNVVYVALVFLSLGNSLWMLVILYSRNSRVDV 81
QY 64 YILNLVAADFLFSGHIGSPL--RLINIRHPISKILSPVMTFPYFIFGLSMLSAIS 121
Db 82 YILNLAMAP-AFCPDHAYLGRQKRLDFTPLCKVSLVKEVNFYSGILLACISVDY 140
QY 122 LSLWPIWYHCRPRYLSSVMCVLLWALSILSLMFWPCDFLFGADSVWC-ETSDFIT 180
Db 141 LAIVQST-RTLTKRHLVFCIGIUALSLULSLPFLFRQVFNSSPVCYDLGHT 199
QY 181 IAWLFLCVLV-----CGSSLLVLRILC-GSRKMPRLRYV-----TILLTVLVF 225
Db 200 AKW---CMVLRILPHTFGFILPLVWMLFCYGTLLTFLQAEHQKRAMRVIFAVLIF 255
QY 226 LLGLPFG-----IQWALFSRIHLDWKVLFCHVHLVSIPLSALNSANPIIY 272
Db 256 LLCWLPYNLVLLADTLMTHTVIOETCQRNELDRALDATEI-----LGLFHSCLNP 309
QY 273 FFVGSFRQNRQNL--LKLVLQAL 295
Db 310 AFIG-----QNFNGFLKMLAARGL 329
RESULT 9
A53611
interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C>Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37898; I38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J: Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B and human interleukin-8 receptor type A.
A:Reference number: I37898; MUID:95014476; PMID:7929358
A:Accession: I37898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803

A:Accession: I38712
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RES2>
A:Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873
11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID
R:Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J: Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 rec
A:Reference number: A53611; MUID:94209273; PMID:7512557
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptc
A:Reference number: A39446; MUID:91368200; PMID:1891716
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, i
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:127868; OMIM:146928
A:Map position: q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 13.4%; Score 226.5; DB 2; Length 360;
Best Local Similarity 26.3%; Pred. No. 1.3e-11;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;
QY 19 BEPCYQKTLSPFG-----LTCIVSLVALTGNA--VVLWLLGCRMRNAVSIYILNLVAAD 72
Db 35 DAAPCEPESELEINKFYVVIYALVFLSLGNSLWMLVILYSRVSRTVDVILNLALAD 94
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFPYFIFGLSMLSAIS 117
Db 95 LLFALTLPWAASKVNGWIFGTLC-----KVVSLLKEVNFYSGILLACIS 141
QY 118 TERCLSLNIPWYHCR-----PRYLSSVMCVLLWALSILSLMFWPCDFLFGADSVWC 173
Db 142 VDRYLAIV-----HATRTLTQKRYLVKFCISLWGLSLLLALPVLFRRTVYSSNVSPAC 196
QY 174 -ETSDFITIAWLFLCVV--LCGSSLLVLRILC-GSRKMPRLRYV-----TILLT 221
Db 197 YEDMGNTANWRMLLRILPQSPGFIVELLINLFCYGTLLTFLKAHQKRAMRVIFAV 256
QY 222 VLVFLLCGLPFG-----IQWALFSRIHLDWKVLFCHVHLVSIPLSALNSAN 268
Db 257 VLIFLLCWLPYNLVLLADTLMTHTVIOETCQRNELDRALDATEI-----LGLFHSCLN 310
QY 269 PIIFYFVG-SFR 279
Db 311 PLIYAFIQKFR 322
RESULT 10
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Polco, E.; Navari
J: Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294; PMID:8175642
A:Accession: A53752
A:Status: preliminary


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Query Match      12.9%; Score 217; DB 2; Length 351;
Best Local Similarity 25.7%; Pred.No. 7.8e-11;
Matches         88; Conservative 60; Mismatches 116; Indels 78; Gaps 18;
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CY 13 TPNGREETPCYKOTLTFTGTCTCVSLVAL-----TGNVAVLWTLGCRMRNAVSIY 64

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Db      298  ILSVANS CANBILYGFUS-----DNFRSRQVRLCRLCCLEGGAGNAEEPLDYAT 349
QY      319  RLE 321
        |
Db      350  ALK 352

Search completed: July 4, 2004, 08:46:02
Job time : 27 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 07:23:28 ; Search time 19 seconds
(without alignments)
882.452 Million cell updates/sec

Title: US-09-787-879c-1

Perfect score: 1688
Sequence: 1 MDSTIPVLGTETLPINGREE.....EGGWLPOETLTLSSGRLEQ 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	461	27.3	378	1	MAS_HUMAN
2	446.5	26.5	324	1	MAS_RAT
3	430.5	25.5	325	1	MAS_HUMAN
4	428.5	25.4	324	1	MAS_MOUSE
5	409	24.2	343	1	MRGF_HUMAN
6	372	22.0	343	1	MRGF_MOUSE
7	371	22.0	343	1	MRGF_RAT
8	255.5	15.1	395	1	GP44_HUMAN
9	246	14.6	349	1	FML2_PANTR
10	244	14.5	349	1	FML2_PONPY
11	244	14.5	353	1	FML2_HUMAN
12	240	14.2	355	1	IL8A_RABIT
13	239	14.2	349	1	FML2_GORGO
14	236.5	14.0	382	1	GP44_MOUSE
15	231	13.7	349	1	FML2_MACACA
16	228.5	13.5	345	1	CSAR_CAVPO
17	226.5	13.4	360	1	IL8B_HUMAN
18	225.5	13.4	353	1	IL8B_MACMU
19	225	13.3	348	1	FML1_PONPY
20	222	13.2	353	1	IL8B_GORGO
21	220	13.0	358	1	IL8B_RABIT
22	219.5	13.0	353	1	IL8B_PANTR
23	219.5	13.0	369	1	SSR2_MOUSE
24	219.5	13.0	369	1	SSR2_RAT
25	219	13.0	348	1	FML1_GORGO
26	217	12.9	351	1	FML1_HUMAN
27	215	12.7	381	1	GP34_HUMAN
28	215	12.7	381	1	GP34_PANTR
29	212	12.6	373	1	FML1_HUMAN
30	211	12.5	348	1	FML1_PANTR
31	211	12.5	353	1	BRB1_PIG
32	211	12.5	375	1	GP34_MOUSE
33	210.5	12.5	388	1	SSR4_HUMAN

34	210	12.4	473	1	CSAR_RAT	O55197	rattus norv
35	209.5	12.4	363	1	SSR5_RAT	P30938	rattus norv
36	207	12.3	350	1	CSAR_RABIT	Q9tuel	oryctolagus
37	207	12.3	395	1	PAR4_RAT	Q92080	rattus norv
38	206	12.2	348	1	FML1_MACMU	P79190	macaca mula
39	206	12.2	350	1	IL8A_GORGO	P55919	gorilla gor
40	206	12.2	369	1	SSR2_PIG	P34994	sus scrofa
41	205.5	12.2	349	1	IL8A_RAT	P70612	rattus norv
42	205.5	12.2	355	1	GPRI_HUMAN	P46091	homo sapien
43	205.5	12.2	384	1	SSR4_RAT	P30937	rattus norv
44	205	12.1	333	1	CXC1_HUMAN	P46094	homo sapien
45	205	12.1	347	1	P2YC_MOUSE	Q9cpv9	mus muscullu

ALIGNMENTS

RESULT 1

MRG_HUMAN	ID	MRG_HUMAN	STANDARD;	PRT;	378 AA.
AC	P35410;				
DT	01-JUN-1994	(Rel. 29, Created)			
DT	01-JUN-1994	(Rel. 29, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Mas-related G protein-coupled receptor MRG (MAS-R) (MAS1-like).				
GN	MAS1L OR MRG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92130987; PubMed=1723144;				
RA	Monnot C., Weber V., Stinnakre J., Bihoreau C., Teutsch B., Corvol P., Clauser E.;				
RT	"Cloning and functional characterization of a novel mas-related gene, modulating intracellular angiotensin II actions.";				
RL	Mol. Endocrinol. 5:1477-1487(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Whitaker H.;				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.				
CC	Mas subfamily.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL;	S78653;	AAB21255.1;	--	
DR	EMBL;	AL035542;	CAB44503.1;	--	
DR	PIR;	A39485;	A39485.		
DR	Genew;	HGNC:13961;	MAS1L.		
DR	MTM;	607235;	--		
DR	GO;	GO:0016021;	C:integral to membrane;	NAS.	
DR	GO;	GO:0004930;	F:G-protein coupled receptor activity;	NAS	
DR	GO;	GO:0007186;	P:G-protein coupled receptor protein signalin. . .	NAS.	
DR	InterPro;	IPR000276;	GPCR Rhodopsin.		
DR	PRINTS;	PR00237;	GPCR RHODOPSIN.		
DR	PROSITE;	PS00237;	G PROTEIN RECP F1_1;	1.	
DR	PROSITE;	PS0262;	G PROTEIN RECP F1_2;	1.	
DR	G-protein coupled receptor; Transmembrane; Glycoprotein.				
KW	DOMAIN 1 77 EXTRACELLULAR (POTENTIAL).				
FT	DOMAIN	78	101		
FT	TRANSMEM	102	109		
FT	DOMAIN	110	136		
FT	TRANSMEM	117	154		
FT	DOMAIN	137	154		
FT	TRANSMEM	155	169		

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FT DOMAIN 170 191 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 192 207
FT DOMAIN 208 221 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 222 248
FT TRANSMEM 249 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 286
FT TRANSMEM 287 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 317
FT TRANSMEM 318 378
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 378 AA; 42410 MW, 508A606294561474 CRC64;

Query Match 27.3%; Score 461; DB 1; Length 378;
Best Local Similarity 37.9%; Pred. No. 8.5e-27;
Matches 107; Conservative 56; Mismatches 81; Indels 38; Gaps 10;

QY 36 IVSLVLTGNVAVLLGCRMRNAVSIYILNVAADFLPLSGHIICSPRLINIR----91
DB 84 LVSLGVLNGTVFVLLCCG-ATNPYMYVILHLVAADVIL-----CCSAGVGLQVLLTY 138

QY 92 HPI-----SKILSPVMTFFYIGLSMLSAISTERCLSLIPWYHCRPRYLSSVMCV 144
DB 139 HGVVFFIPDFLAISP----ESFEVCLCLLVAISTERCVCLVFPFIWYRCHRPKYTSNVCT 195

QY 145 LLWALSLLRSILEWMFCDFLFGSADSVWCETSD---FTIAML--VFLCVLGGSLVLL 199
DB 196 LINGLPCINIVKSLFTY-----WKVKACVFLKSLGFLPHAILSLVMCVSLLTL 247

QY 200 VRILGSRKMLPRLYVITLLTVLVLGCLPGFIQWALFSRIHLWDKVLFCVHVLVSIF 259
DB 248 IRLCCSQQKATRVAVVQISAPMFLWALPLSV-----APLITDFKMFVTSYLISLF 302

QY 260 LSAINSSANPIIYFFVGSFQRQNRQNLKVLQALODTPEV 301
DB 303 L-IINSSANPIIYFFVGSRRKRKESLRVILQALADPEV 343

RESULT 2
MAS_RAT
ID MAS_RAT STANDARD; PRT; 324 AA.
AC P12526;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MAS proto-oncogene.
GN MAS1 OR MAS-1 OR MAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=88276953; PubMed=2455902;
RA Young D., O'Neill K., Jessell T., Wigler M.;
RT "Characterization of the rat mas oncogene and its high-level expression in the hippocampus and cerebral cortex of rat brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5339-5342 (1988).
CC -!- FUNCTION: Not known.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- CAUTION: Was originally thought to be a receptor for angiotensin II.
CC
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CC
CC EMBL; J03823; AAA4573.1; -
DR

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DR PIR; A31816; TVRTAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PS00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein; Proto-oncogene.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 127 3 (POTENTIAL).
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 171 4 (POTENTIAL).
FT DOMAIN 172 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 6 (POTENTIAL).
FT DOMAIN 245 262 7 (POTENTIAL).
FT TRANSMEM 263 324 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 284 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 324 AA; 37130 MW, AD810229BF1E7D36 CRC64;

Query Match 26.5%; Score 446.5; DB 1; Length 324;
Best Local Similarity 38.0%; Pred. No. 8.4e-26;
Matches 108; Conservative 57; Mismatches 96; Indels 23; Gaps 9;

QY 37 VSLVLTGNVAVLLGCRMRNAVSIYILNVAADFLFGHIICS-----PRLINIR 91
DB 41 ISPLGFVENGILLWFLCFMRNPNFTVITHLSADIALLFCIFILSDVADLYELSSGH 100

QY 92 HPIKILSPVMTFFYIGLSMLSAISTERCLSLIPWYHCRPRYLSSVMCVLWALS 151
DB 101 YTVITLSVTFPGYITGLYLLTAISVERCLSVLPYIWRCHRPKHOSAFVALLWALSC 160

QY 152 LRSILEWMFCDFLFGSADSVWCETSD-----FTI-ANLFLCVLGGSLVLLVRLC 204
DB 161 LVTINWYVVC--IDSGEES--HSQSDCAVIFIALSLFVFTPLMLV-SSTLVWVKRK 215

QY 205 GSRKNPLTRLVYVITLLTVLVLGCLPGFIQWALFSRIHLWDKVLFCVHVLVSIFLSALN 264
DB 216 NTWASHSSKLYIVIMVTIIIFLIPMPMRVLYLYEY--WST-FGNLHNISLLFSTIN 271

QY 265 SSANPIIYFFVGSFQRQNRQNLKVLQALQD--TPEVDEGGG 306
DB 272 SSANPIIYFFVGSKKKRFRESLKVILTRAPKDEWQPRQEGNG 315

RESULT 3
MAS_HUMAN
ID MAS_HUMAN STANDARD; PRT; 325 AA.
AC P04701;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MAS proto-oncogene.
GN MAS1 OR MAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=86218084; PubMed=3708691;
RA Young D., Waechter G., Birchmeier C., Fasano O., Wigler M.;
RT "Isolation and characterization of a new cellular oncogene encoding a protein with multiple potential transmembrane domains.";
RL Cell 45:711-719 (1986).

```

RP POSSIBLE FUNCTION.
RX MEDLINE=88334724; PubMed=3419518;
RA Jackson T.R., Blair L.A.C., Marshall J., Goedert M., Hanley M.R.;
RL "The mas oncogene encodes an angiotensin receptor.";
RT Nature 335:437-440(1988).
CC -!- FUNCTION: Not known.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DISEASE: The MAS oncogene has a weak focus-inducing activity in
transfected NIH 3T3 cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- CAUTION: Was originally (Ref.1) thought to be a receptor for
angiotensin II.
CC
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M13150; AAA36199.1; -;
CC PIR; A01375; TVHUAS.
CC Genew; HGNC:6899; MAS1.
CC MIM; 165180; -;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004945; F: angiotensin type II receptor activity; TAS.
CC GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
CC GO; GO:0008283; P: cell proliferation; TAS.
CC GO; GO:0007345; P: embryogenesis and morphogenesis; TAS.
CC GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Proto-oncogene.
FT DOMAIN 1 36 1 (POTENTIAL).
FT TRANSMEM 37 61
FT DOMAIN 62 65
FT TRANSMEM 66 86
FT DOMAIN 87 104
FT TRANSMEM 105 128
FT DOMAIN 129 149
FT TRANSMEM 150 172
FT DOMAIN 173 185
FT TRANSMEM 186 206
FT DOMAIN 207 224
FT TRANSMEM 225 245
FT DOMAIN 246 263
FT TRANSMEM 264 284
FT DOMAIN 285 325
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 325 AA; 37465 MW; 3368E7B174744883 CRC64;
Query Match 25.5%; Score 430.5; DB 1; Length 325;
Best Local Similarity 37.9%; Pred. No. 1.2e-24;
Matches 103; Conservative 56; Mismatches 94; Indels 19; Gaps 8;
QY 37 VSLVLTGNVVLWLLGCMRNANVILNVLVAADFLLFSLGHICS-----PRLNLR 91
DB 42 ISFGVGVENGILLWFLCFMRNPNPTVYTHLSIADISLLFCIFLSIDYALDYELSSGH 101
QY 92 HPISKILSVMTFPFPIGLMSAISLSTERCLSIPLWYCHRRPYLSVMCVLLWALS 151
DB 102 YVTIVLSVTFEGYNTGLYLTALSVRELCLSVLPYWRCHRPKYQALVCALLWALSC 161
QY 152 LRSILEWMEFC---DFLPSGADSVNCE-TSDFTTI-AMLVFCVVLGSSVLVRLICG 205

DB 162 LVTMEYVMCIDREESHNRD---CRAVIFAIILSLFVFTPLMLV-SSTILVVKIRKN 217
QY 206 SRKMPLTRLYVTILTLVLVFLCGLFQIOWALFRIHLDMKVLFCVHLVSIFLSALNS 265
DB 218 TWASHSSKLYIVIMVTIIFLIFAMPBRLLYLLYYEY---NST-FGNLHHISLLESTINS 273
QY 266 SANPIYFVGSFQROQRONKLVQLQALQD 297
DB 274 SANPFYFVGSKKRKFESLKVVLTRAFKD 305
RESULT 4
MAS_MOUSE STANDARD; PRT; 324 AA.
ID MAS_MOUSE
AC P30554; O35944;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MAS proto-oncogene.
GN MAS1 OR MAS-1 OR MAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=95094925; PubMed=8001672;
RA Metzger R., Bader W., Ludwig T., Berberich C., Bunnemann B.,
RA Ganten D.;
RT "Expression of the mouse and rat mas proto-oncogene in the brain and
peripheral tissues.";
RL FEBS Lett. 357:27-32(1995).
RN [2]
RP SEQUENCE OF 1-25 FROM N.A.
RC STRAIN=BCBA; TISSUE=Testis;
RX MEDLINE=97422605; PubMed=9286631;
RA Schweifer N., Valk P.J., Deibel R., Cox R., Francis F.,
RA Meier-Ewert S., Lehrach H., Barlow D.P.;
RT "Characterization of the C3 YAC contig from proximal mouse chromosome
17 and analysis of allelic expression of genes flanking the imprinted
Igf2r gene.";
RL Genomics 43:285-297(1997).
CC -!- FUNCTION: Not known.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- CAUTION: Was originally thought to be a receptor for angiotensin
II.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X67735; CAA47964.1; -;
CC EMBL; U96273; AAB69120.1; -;
CC PIR; S51001; S51001.
CC MGD; MGI:96918; Mas1.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Proto-oncogene.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).


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FT TRANSMEM 104 127 3 (POTENTIAL)
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 149 171 4 (POTENTIAL)
FT DOMAIN 172 184 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 185 205 5 (POTENTIAL)
FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 224 244 6 (POTENTIAL)
FT DOMAIN 245 262 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 263 283 7 (POTENTIAL)
FT DOMAIN 284 324 CYTOPLASMIC (POTENTIAL)
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL)
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL)
FT CARBOHYD 21 21 N-LINKED (GLCNAC. .) (POTENTIAL)
FT CONFLICT 19 19 S -> I (IN REF. 2)
SQ SEQUENCE 324 AA; 36904 MW; 24F4AB729936016F CRC64;

Query Match 25.4%; Score 428.5; DB 1; Length 324;
Best Local Similarity 37.7%; Pred. No. 1.7e-24;
Matches 107; Conservative 56; Mismatches 98; Indels 23; Gaps 9;

QY 37 VSLVALTGNVAVLWLLGCRNRNAVSIYILNVAADFLFSGHHICS-----PLRLINIR 91
DB 41 ISPLGFVENGILLWFLCFMRNRNPFTVYITHLSMADISLLFCIFILSIDYALDYELSSGH 100
QY 92 HPISKILSPWTPPYFTGLSMLSAISTERCLSLNPIWYHCRPRYLSSVMCVLLWALS 151
DB 101 HYITVLSVTLFQYNTGLYLLTAISVERCLSVLPYWTSHRPHQSAFVCAALLCASC 160
QY 152 LRSILEMWFCDLFPAGDSVWCETSD-----FTTI-AMLVFLCVLVCGSSLLVLRILC 204
DB 161 LVITMEYVMC--IDSGES--HRSDCRAVIFIALISFLVTFPLMLVSS--ILVVKIRK 215
QY 205 GSRKMPITRYVITLLVFLVLCGLPFGIQWALFSLRHLDKVLFCFHVHLVSLFISALN 264
DB 216 NTWASHSKLYIVMTVITIFLIPAMPVRLVLYEY---WSA-FGNLHNISLLESTIN 271
QY 265 SSANPIYFFVGSFQRONQNLKVLQALQD--TPEVDEGGG 306
DB 272 SSANPIYFFVGSKKKRFRESLKVLTFRKDEMQRQEGNG 315

RESULT 5
MRGF_HUMAN STANDARD; PRT; 343 AA.
AC O96AM1: OSNBKA;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mas-related G protein-coupled receptor MRGF (Mas-related gene F protein).
GN MRGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isogai T.,
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsden K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Orphan receptor. May bind to a neuropeptide and may
CC regulate nociceptor function and/or development, including the
CC sensation or modulation of pain (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.

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EMBL: AK075450; BAC11628.1; -
EMBL: BC016964; AAH16964.1; -
WIM: 607233; -
InterPro: IPR000276; GPCR_Rhodopsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS: PR00237; GPCRHOPOPSN.
PROSITE: PS00237; G-PROTEIN RECP F1_1; 1.
PROSITE: PS0262; G-PROTEIN RECP F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 44 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 45 66 1 (POTENTIAL)
FT DOMAIN 67 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 104 2 (POTENTIAL).
FT DOMAIN 105 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 144 3 (POTENTIAL).
FT DOMAIN 145 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 220 5 (POTENTIAL).
FT DOMAIN 221 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 263 6 (POTENTIAL).
FT DOMAIN 264 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 294 7 (POTENTIAL).
FT DOMAIN 295 343 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 16 16 K -> R (IN REF. 1).
SQ SEQUENCE 343 AA; 38171 MW; 169A649F5B38F154 CRC64;

Query Match 24.2%; Score 409; DB 1; Length 343;
Best Local Similarity 34.9%; Pred. No. 4.7e-23;
Matches 103; Conservative 51; Mismatches 117; Indels 24; Gaps 8;

QY 33 LTCIVSLVALTGNVAVLWLLGCRNRNAVSIYILNVAADFLFSGHHICSLR----- 86
DB 53 LLCLCGLV---GNGLVLPFFGFSIKRNPFSYFLHLASADVGLFSKAVFIINTGGFLG 109
QY 87 -LINTRHPIISKILSPWTPPYFTGLSMLSAISTERCLSLNPIWYHCRPRYLSSVMCVL 145
DB 110 TADYIRSVCRVLGLCM---FLTGVSLLPAVSAERCAVIFPAPWYRRPKRLSAVVAL 166
QY 146 LMAVLSRLSILEMWFCDLFPAGDSVWCETSD-FTTIAMLVFLCVLVCGSSLLVLRILC 204
DB 167 LMVLSLLVTLNHYFCVFLGRGAPGACACRHMDFLGLILLFLCCPLMVLPCALILHVEC 226

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QY 205 GSRKMPLT-RLYVTILTVLVFLGCLPFGIQLWALFSRIHLDK--KVLFCVHVLVSIFLS 261
DB 227 RARRQRSAKLNHVLAWSVFLVSSIVLGDWELF-----WVFQIPAPPPYVTDLCI 280
QY 262 ALNSSANPIYFFVGSFRQRNQNLKVLQRALQDTPVEDGGWLPQBF-TLEL 315
DB 281 CINSSAKPIVFLAGDKSQRLEWPLRVFQALRDGAELGEAGGSGTPTVTVMEM 335

RESULT 6
MRGF_MOUSE
ID MRGF_MOUSE STANDARD; PRT; 343 AA.
AC Q8VCJ6; Q912B6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mas-related G protein-coupled receptor MRGF (Mas-related gene F
DE protein).
GN MRGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Vax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 25-343 FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RA "A diverse family of GPCRs expressed in specific subsets of
RT nociceptive sensory neurons.";
RL Cell 106:619-632(2001).
CC -!- FUNCTION: Orphan receptor. May bind to a neuropeptide and may
CC regulate nociceptor function and/or development, including the
CC sensation or modulation of pain.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.
CC
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CC
CC EMBL; BC019711; AAH19711.1; --
CC DR EMBL; AY042211; AAK91802.1; --
CC MGI; 2384823; BC019711.

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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 44
KW EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 45 66
FT DOMAIN 67 82
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 104
FT DOMAIN 105 123
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 144
FT DOMAIN 145 160
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 181
FT DOMAIN 182 198
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 220
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 221 241
FT TRANSMEM 242 263
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 264 273
FT TRANSMEM 274 294
FT DOMAIN 295 343
FT CARBOHYD 4
SQ SEQUENCE 343 AA; 38522 MW; 358ED59587C9A317 CRC64;

Query Match 22.0%; Score 372; DB 1; Length 343;
Best Local Similarity 33.8%; Pred. No. 2.3e-20;
Matches 101; Conservative 53; Mismatches 113; Indels 32; Gaps 11;

QY 33 LTCIVSLVALTGNAVVLMLGCRMRNAVSIYILNVAADFSLSGHICSPRLIN--- 89
DB 53 LCLCGLV---GNGLVJWFQFSIKRTPFSYFLHLASADGMFLSKAV---IALLNMG 106
QY 90 -----IRHPISKILSPVMTFFYIGLSMLSAISTRCILSIWPIWYHRRPRYLSV 141
DB 107 FLGSPDPYIR--VSRIVG-LCTF--FTGVSLPAISIERCVSVIPPTWYRRPKLSAG 162
QY 142 MCVLWALSLRLSILEWFMFCDFLPSGADSVNCTSDFTIAWLVL-CVILCGSSLVLV 200
DB 163 VCALWMLSLFVTSIHNVFCMFLGHEAPGVCRWMDIALGILLFLFCPLVPLALIL 222
QY 201 RILGSRKMPLT-RLYVTILTVLVFLGCLPFGIQLWALFSRIHLDK--KVLFCVHVLVS 257
DB 223 HVECRARRQRSAKLNHVLAWSVFLVSSIVLGDWELF-----WVFQIPAPPPYV 276
QY 258 IFLSALNSSANPIYFFVGSFRQRNQNLKVLQRALQDTPVEDGGWLPQBF-TLEL 315
DB 277 DLICICINSSAKPIVFLAGDKSQRLEWPLRVFQALRDGAELGEAGGSGTPTVTVMEM 335

RESULT 7
MRGF_RAT
ID MRGF_RAT STANDARD; PRT; 343 AA.
AC P23749;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mas-related G protein-coupled receptor MRGF (Mas-related gene F
DE protein) (G protein-coupled receptor RTA).
GN MRGF OR RTA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Aorta;
RX MEDLINE=90222168; PubMed=2109324;
RA Ross P.C., Figler R.A., Corjay M.H., Barber C.M., Adam N.,
RA Marcus D.R., Lynch K.R.;
RA "RTA, a candidate G protein-coupled receptor: cloning, sequencing,
RT and tissue distribution.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056(1990).
CC -!- FUNCTION: Orphan receptor. May bind to a neuropeptide and may

```

CC regulate nociceptor function and/or development, including the
 CC sensation or modulation of pain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: GUT, VAS DEFERENS, UTERUS, AND AORTA BUT ONLY
 CC BARELY DETECTABLE IN LIVER, KIDNEY, LUNG, AND SALIVARY GLAND. IN
 CC THE BRAIN, IT IS MARKEDLY ABUNDANT IN THE CEREBELLUM.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M35297; AAA42087.1; -;
 DR EMBL: M35298; AAA42088.1; -;
 DR FIR: A35639; A35639.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1.1; 1.
 DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 44
 FT TRANSMEM 45 66
 FT DOMAIN 67 82
 FT TRANSMEM 83 104
 FT DOMAIN 105 123
 FT TRANSMEM 124 144
 FT DOMAIN 145 160
 FT TRANSMEM 161 181
 FT DOMAIN 182 198
 FT TRANSMEM 199 220
 FT DOMAIN 221 241
 FT TRANSMEM 242 263
 FT DOMAIN 264 273
 FT TRANSMEM 274 294
 FT DOMAIN 295 343
 FT CARBOHYD 4 4
 SQ SEQUENCE 343 AA; 38364 MW; E4630007770941F4 CRC64;
 Query Match 22.0%; Score 371; DB 1; Length 343;
 Best Local Similarity 33.1%; Pred. No. 2.8e-20;
 Matches 99; Conservative 58; Mismatches 110; Indels 32; Gaps 11;
 QY 33 LTCIVSLVLTGNVAVLVLLGCMRRNNAVSIYILNVAADFLLSGHIICSPLELINIR- 91
 Db 53 LLLCLGLV--GNGLVLFYFGFSIKRTPFSYFLHLASADGIYLFSAV---IALLNMT 106
 QY 92 -----HPTSKILSPVMTTPYFGLSMLSAISTERCLSLWPIWTHCRPRYLSVM 142
 Db 107 FLGSPDPYVRRSVRIG-LCTP--FAGVSLLPALISIERCVSIFPPMYWYRRPKRLSAGV 163
 QY 143 CVLLWALSLSRSILEMFCDFLFGSADSVWCSTSDFTIAMLVF--LCVWLCSGLVLLV 200
 Db 164 CALLWLLSLFVTSIHNVYFCWFLGHEASGACLNMD-ISIGILLPFLFCPLVPLALIL 222
 QY 201 RILCGSKKPLT-RLVYVILLVYVFLLCGLFPGQWALFGRHLDW--KVLFGCHVLVS 257
 Db 223 HVECRARRRQRSKALNHVLAIVSVFLVSSIVLGGIDWFLF-----WVFQIPAPPEVYT 276
 QY 258 IFLSALNSANPIIYFVGSFRQQRNQLKVLQRLQDTPTVEDEGGWLPQF-TLEL 315
 Db 277 DLLCICINSAKPIYVFLAGDRKSQRLWEPLRVVFORALRDGAEPDGAASSTPNTVTNEM 335
 RESULT 8
 GP44_HUMAN
 ID GP44_HUMAN
 AC Q9Y5Y4; O94765; PRT; 395 AA.

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative G-protein-coupled receptor GPR44 (Chemoattractant receptor-
 DE homologous molecule expressed on Th2 cells).
 GN GPR44 OR CRTH2 OR DLIR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99156852; PubMed=10036181;
 RA Marchese A., Sawadargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
 RA Im D.S., Lynch K.R., George S.R., O'dowd B.F.;
 RT "Discovery of three novel orphan G-protein-coupled receptors.";
 RL Genomics 56:12-21(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99138803; PubMed=9973380;
 RA Nagata K., Tanaka K., Ogawa K., Kemmotsu K., Imai T., Yoshie O.,
 RA Abe H., Tada K., Nakamura M., Sugamura K., Takano S.;
 RT "Selective expression of a novel surface molecule by human Th2 cells
 RT in vivo.";
 RL J. Immunol. 162:1278-1286(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Methner A., Schroeder S.;
 RT "Tissue expression and chromosomal organization of a novel G protein-
 RT coupled receptor.";
 RL Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL: AF118265; AAD21055.1; ALT_INIT.
 DR EMBL: AB008535; BAA74518.1; -;
 DR EMBL: AF144308; AAD34539.1; -;
 DR Genew; HGNC:4502; GPR44.
 DR MIM: 604837; -;
 DR GO; GO:0005687; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0007185; F:G-protein coupled receptor protein signalin. . .; TAS.
 DR GO; GO:0006955; F:immune response; TAS.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1.1; 1.
 DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 33
 FT TRANSMEM 34 56
 FT DOMAIN 57 67
 FT TRANSMEM 68 89
 FT DOMAIN 90 106
 FT TRANSMEM 107 127
 FT DOMAIN 128 146
 FT TRANSMEM 147 168
 FT DOMAIN 169 210
 FT TRANSMEM 211 231
 FT DOMAIN 232 247
 FT TRANSMEM 248 269
 FT DOMAIN 270 288

FT TRANSMEM 289 308 7 (POTENTIAL).
 FT DOMAIN 309 395 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 104 182 POTENTIAL.
 FT CONFLICT 375 GSCAASPTGPNALSTSS -> VOLRSVPADGPPPGA
 FT SCHLELEPGPRRAALTRESITRVFNSISGLLPQ (IN
 FT REF 1).
 FT SEQUENCE 395 AA; 43239 MW; 9DBBB53B2008C1D1 CRC64;
 Query Match 15.1%; Score 255.5; DB 1; Length 395;
 Best Local Similarity 25.9%; Pred. No. 8.1e-12;
 Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;
 QY 36 IVSLVATGNVAVLWLLGCRNRNAVSIYILNVADEL-----FLS-----G 78
 DB 41 LASLGLVGVGVVGGCRQVTVVTVVHLALSDDLASLPFFTYFVAVGSHWELG 100
 QY 79 HIICFLRLINIRHPISKILSPVMTFFYFIFGLSLSAISTERCLSIILPIWYHCRPRYL 138
 DB 101 TTF-----KLHSSIFELNMFASGFLLSAIDRCLQVVRPVWAQHRTVAA 147
 QY 139 SSMCVLWALSLLSIENWFCDFLPGASVWC-----E 174
 DB 148 AHKVCVLWALAVLNTVPYFVFRDTISLDGRIMCYNVLLNPPDRDATCNSRQAALA 207
 QY 175 TSDFTITIAWLVLCVGLCGSSLVILVRILCGSRKMPRLVYVTLITLVFLVLCGLPFI 234
 DB 208 VSKFL-LAFVPLAIASHAAVSL-RLQHRGRRP-GRFVRLVAAVAAALCWGPYHV 264
 QY 235 QWALSRTH-----LWKVLFCHVHLVSLFSLA-----NSSANPIIYFVGSFRQNR 284
 DB 265 FSLLEARAHANFGLRPLVWRLG-----PFVTSIAFNSVANPVLVLCPPMLAKLR 316
 QY 285 ONKLVLORALQDTEVEDEG 305
 DB 317 RSLRTVLSVLDSELGAG 337

RESULT 9
 FML2 PANTR
 ID FML2 PANTR STANDARD; PRT; 349 AA.
 AC P79243;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
 DE (Fragment).
 GN FPRU2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96421539; PubMed=8824156;
 RA Alvarez V., Coto B., Selen P., Gouzalet-Koccs S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in
 non-human primates."
 RL Immunogenetics 44:446-452(1996).
 CC -!- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 which are powerful neutrophils chemotactic factors. Binding of
 FMLP to the receptor causes activation of neutrophils. This
 response is mediated via a G-protein that activates a
 phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC ENBL; X97743; CAA66327.1; .
 DR InterPro; IPR000276; GPCR Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 KW DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 50 1 (POTENTIAL).
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 62 83 2 (POTENTIAL).
 FT TRANSMEM 84 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 121 3 (POTENTIAL).
 FT TRANSMEM 122 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 162 4 (POTENTIAL).
 FT TRANSMEM 163 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 5 (POTENTIAL).
 FT TRANSMEM 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 266 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 267 286 6 (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT TRANSMEM 307 >349 POTENTIAL.
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 98 176 POTENTIAL.
 FT NON TER 349
 FT SEQUENCE 349 AA; 882798C72915383 CRC64;
 Query Match 14.6%; Score 246; DB 1; Length 349;
 Best Local Similarity 24.3%; Pred. No. 3.6e-11;
 Matches 83; Conservative 75; Mismatches 111; Indels 72; Gaps 15;
 QY 14 PINGEE-----TPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCRMRNAVSI 65
 DB 8 PLNETEVLPEPAGHTVLMIFSLVHGVTFFGVL---GNGLVWVAGFRMTWTNTICY 64
 QY 66 LNLVAADELFLSGHIICSPRLINI-----RHP-----ISKILSPVMTFFYFIFGLSLSA 117
 DB 65 LNLADAFSFA---ILPFMVSVAMREKPPGSELCVKLVHVMIDINLFVSVYLITIA 120
 QY 118 TERCLSIILPIWYHCRPRYLSVMCVLWALSLASILEWMP-----CDFLF 165
 DB 121 LDRICICVLHPAAQNHRTWSLAKRVMTGLWTLTLPNFIFMTTIRTNNGDYCINP 180
 QY 166 SGADSVKCT-----SDFITIAMLVLCVGLCGSSLVILVRILC-----G 205
 DB 181 ----AFWGDTAVERLNVFIMAKVFLILHFIIGFSPMSIITVCYGIAAKIHNRHMKS 236
 QY 206 SRKMPRLVYVTLITLVFLVLCGLPF---GIQWALFSR---IHLQWVLFCHVHLVSIF 259
 DB 237 SR--PL-RVFAAV---VASPFICWFFYELIGILMAVLMKMLNGYKIILVILNPTS-S 289
 QY 260 LSAINSSANPIIYFVGSFRQNRONKLVLORALQDTE 300
 DB 290 LAFNSCLNELLVFMGRNFOERLIRSLFTSLERALTVPD 330
 RESULT 10
 FML2 PONPY
 ID FML2 PONPY STANDARD; PRT; 349 AA.
 AC P79237;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
 DE (Fragment).
 GN FPRU2.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96421539; PubMed=8824156;
RA Alvarez V., Coro E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RT non-human primates."
RL Immunogenetics 44:446-452(1996).
CC -|- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC -|- PHOSPHATIDYLINOSITOL-calcium second messenger system.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL: X97741; CRA66325.1; ..
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR0237; GPCRHOPOPSN.
DR PROSITE: PS00237; G PROTEIN RECF F1.1; 1.
DR PROSITE: PS00262; G PROTEIN RECF F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 50 1 (POTENTIAL).
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 266 6 (POTENTIAL).
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC...) (POTENTIAL).
FT DISULFID 98 176 POTENTIAL.
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39423 MW; C8298D23395EECB CRC64;

Query Match 14.5%; Score 244; DB 1; Length 349;
Best Local Similarity 24.2%; Pred. No. 5e-11;
Matches 82; Conservative 74; Mismatches 115; Indels 68; Gaps 14;

QY 14 PINGRES-----TPCYQTSLFTGLTGVISVALTGNVAVLWLLGRCMRNAVSIYI 65
DB 8 PLNSESEVLPBAGHTVWIFSLVGVHTFIFGVL---GNGLVWAGFRMTVTNVCY 64
QY 66 LNVAAQFLFSGHHICSPALINI-----RHP-----ISKILSPWTFPPYIGLSMLSAT 117
DB 65 LNLALADPFSFA---LIPFMVSVAMREKWPFGTFLCKLVHVMIDINLFVSYLITIA 120
QY 118 TERGLSILWPTWYHCRPRVYSSVWCVLLWALSRLRSILEWMP-----CDFLF 165
DB 121 LDRICVLHPAKAQNRTMSLAKVMGLMTLAILVLPNFIFWTITKNGDYCIENF 190
QY 166 SGASVWCET-----SPITIANVLVLCVLCGSSIVLVRLCG-----SR 207
DB 181 ----PFWGDTAVESLNAPITWKGKVLILHFIIGFSPMPSIITVCYIIAAKIHNNMIKS 236

QY 208 KMPLTRLYVTLLTLVFLLCGLPF---GIQWALFSR---IHLDKVLFCHVHLVSIPLS 261
DB 237 SSPL-RVFAAV--VASFFICWFFYELIGILMAVLKEMLLNGKYKIILLNPTS-SLA 291
QY 262 ALNSANPIIYFFVGSFRQNRQNLKLVLRALQDTPE 300
DB 292 FFNSCLNPIIYVFLGNSFQBELIRSLPTSLEALTEVPD 330

RESULT 11
FML2_HUMAN
ID FML2_HUMAN STANDARD; PRT; 353 AA.
AC P25089;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2).
GN FPR12 OR FPR11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307681; PubMed=1612600;
RA Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;
RT Mapping of genes for the human C5a receptor (C5AR), human FMLP
RT receptor (FPR), and two FMLP receptor homologue orphan receptors
RT (FPRH1, FPRH2) to chromosome 19."
RL Genomics 13:437-440(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94256976; PubMed=8198572;
RA Durstin M., Gao J.-L., Tiffany H.L., McDermott D., Murphy P.M.;
RT "Differential expression of members of the N-formylpeptide receptor
RT gene cluster in human phagocytes."
RL Biochem. Biophys. Res. Commun. 201:174-179(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org)."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
TX TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.N., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 KW DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 41 67 1 (POTENTIAL).
 FT DOMAIN 68 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 92 2 (POTENTIAL).
 FT DOMAIN 93 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 138 3 (POTENTIAL).
 FT DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 160 184 4 (POTENTIAL).
 FT DOMAIN 185 204 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 205 232 5 (POTENTIAL).
 FT DOMAIN 233 247 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 248 270 6 (POTENTIAL).
 FT DOMAIN 271 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 313 7 (POTENTIAL).
 FT DOMAIN 314 355 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 7 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 115 192 BY SIMILARITY.
 FT CONFLICT 90 111 DLFPALTPWAVSKGHWIFG ->
 FT CONFLICT 146 147 PAFCDPDAVLRGRGRRLDFR (IN REF. 2).
 FT CONFLICT 204 204 HA -> QS (IN REF. 2).
 FT CONFLICT 287 288 R -> C (IN REF. 2).
 FT CONFLICT 287 288 DI -> EL (IN REF. 2).
 SQ SEQUENCE 355 AA; EFE49ACB9D1E0F21 CRC64;
 Query Match 14.2%; Score 240; DB 1; Length 355;
 Best Local Similarity 27.4%; Pred. No. 9.9e-11;
 Matches 92; Conservative 57; Mismatches 109; Indels 78; Gaps 17;
 QY 10 TELTPINGREETPC--YKQTLG---FTGLTCIVSLVALTGN-VVLWLLGCMRRNAVSI 63
 Db 23 TGMPPVE-KOYSPCLVVTQTLNKKVYVVALVFLSLGSLVMLVILYSRNRSVTDV 81
 QY 64 YILNVAADFLPSCHICSPRLIN-----TRHPISKILSPYMTFFPFGLSMLSATS 117
 Db 82 YLLNVAADLFL-----ALTMPIWAVSKGHWIFGTLCKVSLVSKVNFYSGILLACIS 137
 QY 118 TERCLSLWPIVYHCR-----PRYLSVMCVLLWALSLSLSILEWFCDFLFGADSVMC 173
 Db 138 VDRYLAIV-----HATRTLQKHLVKFICLGIWALSLSLSLFLFLFRQVFSNNSSPVC 192
 QY 174 -ETSDFITIAWLVLCV--LGGSSVLVRLIC-GSRKMPRLRV-----TILLT 221
 Db 193 YEDSGHTAKRWVRLRPHPTFTGFIPLVLMFCYGTFLRTLQAHMGQKRAVRVFAV 252
 QY 222 VLVPFLCGLPFGIQWALFSRIHLDWKVLC-----HVHLV-----SIFLS 261
 Db 253 VLIFELCNLPNL-----VLLADTLMRTHVIGETQCRNDIDRALDATEILG 299
 QY 262 ALNSANPIYFFVGSFRQNRQN--LKLVLQAL 295
 Db 300 FLHSLNPIIYAFIG-----QNFNGELKMLAERGL 330
 RESULT 13
 FML2_GORGO STANDARD; PRT; 349 AA.
 AC P79178;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
 DE (Fragment).
 GN FPR12.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OC NCBI_TaxID=95595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96421539; PubMed=8824156;

RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and Csa receptors in
 RL non-human primates.";
 CC Immunogenetics 44:446-452(1996).
 CC -!- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 CC which are powerful neutrophils chemotactic factors. Binding of
 CC FMLP to the receptor causes activation of neutrophils. This
 CC response is mediated via a G-protein that activates a
 CC phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL: X97742; CAA66326.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHO00FSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 50 1 (POTENTIAL).
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 62 83 2 (POTENTIAL).
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 121 3 (POTENTIAL).
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 162 4 (POTENTIAL).
 FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 266 6 (POTENTIAL).
 FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 98 176 POTENTIAL.
 FT NON_TER 349
 SQ SEQUENCE 349 AA; C6ED77CFDE023834 CRC64;
 Query Match 14.2%; Score 239; DB 1; Length 349;
 Best Local Similarity 25.0%; Pred. No. 1.2e-10;
 Matches 85; Conservative 71; Mismatches 114; Indels 70; Gaps 15;
 QY 14 PINGREE-----TPCYKOTLSFTGLTCTVSLVALTGNVVLWLLGCMRRNAVSIYI 65
 Db 8 PLNTEEEVLPSPAGHTVLIWFSLLVHGVTFIFGVLF--GNGLVIVAGVGLTRTNTICY 64
 QY 66 LNLVAADFLF--LSGHICSPRLINIRHP-----ISKILSPVMTFPYFGLSMLSIST 118
 Db 65 LNLVAADFSFSAILLPFHNVSVAMR---EKWFGSLCKLVHVMIDINLFVSYLITIAL 121
 QY 119 ERCLSLPWIYHCRPRYLSVMCVLLWALSLSLSILEWVF-----CDFLFS 166
 Db 122 DRCICVLHPAWAQNHRMTSLAKRVMTGLWILTLPNFIPTTISTNGDTYCIENF- 180
 QY 167 GADSVWCET-----SDFITIAWLVLCVVLGSSVLVRLIC-----GS 206
 Db 181 ----PFGDFAVERLAVFTIMAKVFLILHFIIGFSPMSIIVCYGIIIAKTRHNHMKSS 237
 QY 207 RKMPLTRLYVTILLVVLVFLCGLPF---GIQWALFSR---IHLDMKVLFCFCHVLSIFL 260
 Db 238 R--PL-RVFAAV--VASFFICWFFYELIGILMAVLMKEMLLNGYKIILVLIPTS-SL 290

FT	TRANSMEM	28	50	1 (POTENTIAL).
FT	DOMAIN	51	61	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	62	83	2 (POTENTIAL).
FT	DOMAIN	84	100	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	101	121	3 (POTENTIAL).
FT	DOMAIN	122	140	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	141	162	4 (POTENTIAL).
FT	DOMAIN	163	205	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	206	226	5 (POTENTIAL).
FT	DOMAIN	227	242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	243	266	6 (POTENTIAL).
FT	DOMAIN	267	286	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	287	306	7 (POTENTIAL).
FT	DOMAIN	307	>349	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	10	10	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	DISULFID	98	176	POTENTIAL.
FT	NON_TER	349	349	
SQ	SEQUENCE	349 AA;	39531 MW;	COC92A9E5CDE250C CRC64;
Query Match 13.7%; Score 231; DB 1; Length 349;				
Best Local Similarity 24.2%; Pred. No. 4.4e-10;				
Matches 80; Conservative 74; Mismatches 126; Indels 50; Gaps 12;				
QY	14	PINGREE-----TPCYKQILSFTGLTCIVSLVALTGNVAVLLGCRMRNAVSIYI	65	
Db	8	PLNETEEVLPEPAGHTVLMIFSLLVHGVTFIFQVL---GNGIVIVVAGFRMTRVNTICY	64	
QY	66	LNLVAADFLF---LSGHIICSPRLINIRHP---ISKILSPVMTFPYPFIGLSMLSAIST	118	
Db	65	LNLALADFSALPEHMYVAVNR---EKWFGTFLCKLVHVMIDINLFVSVLITIAL	121	
QY	119	ERCLSIILWPIWYHCRPRYLSSVMCVLLWALSRLSILEWMP-----CDFLPS	166	
Db	122	DRICICVLPFAQNRHTMSLAKVMTGLWILTVLTPNFIEFWTIISTTNGDTCIFNYP	181	
QY	167	-GADSVWCETSDFTITIAWLFLCVLCSGLVLLVRLC-----GSRKMPLTRLYVT	217	
Db	182	FWGDTVVERNVFTIAKVSLLIHFIFGSPIMSITVCYGIIVAKIHKRWTKSRPLH	241	
QY	218	ILLTVL-FLCGLPF---GIQWALFSR---IHLDMKVLFCVHVLVSIPLSALNSSANPI	270	
Db	242	IFTAVVASFFICWFPYELTGILMAVWLKEILLNGKYKIILVLIINPTS-SLAFFNSCLNPS	300	
QY	271	IYFVVGSRQRONKLVLRALQDTPE	300	
Db	301	LYVFMGHNFOERLIRSLPTSLEALTEVPD	330	

Search completed: July 4, 2004, 08:44:11
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:29:04 ; Search time 71 Seconds
(without alignments)
1430.942 Million cell updates/sec

Title: US-09-787-879C-1

Perfect score: 1688

Sequence: 1 MDSTIPVLGTELPINGREE.....EGGWLFPQETLELSGSRLEQ 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1688	100.0	322	4 Q96LB0	Q96LB0 homo sapien
2	1675	99.2	322	4 Q8TDE1	Q8TDE1 homo sapien
3	1606	95.1	322	4 Q8TDE0	Q8TDE0 homo sapien
4	1411	83.6	322	4 Q8TDD9	Q8TDD9 homo sapien
5	1383	81.9	322	4 Q96LB2	Q96LB2 homo sapien
6	1382	81.9	322	4 Q8TDD7	Q8TDD7 homo sapien
7	1382	81.9	322	4 Q8TDD8	Q8TDD8 homo sapien
8	1367	81.0	322	4 Q96LA9	Q96LA9 homo sapien
9	1360	80.6	322	4 Q8TDD6	Q8TDD6 homo sapien
10	989.5	58.6	330	4 Q96LB1	Q96LB1 homo sapien
11	823.5	48.8	323	11 Q7TN42	Q7TN42 rattus norv
12	820.5	48.6	337	11 Q8R4G1	Q8R4G1 rattus norv
13	797	47.2	322	11 Q8CIF3	Q8CIF3 mus musculu
14	782	46.3	304	11 Q7TN49	Q7TN49 rattus norv
15	778	46.1	331	11 Q91YB7	Q91YB7 rattus norv
16	762	45.1	338	11 Q91ZC2	Q91ZC2 mus musculu

17	762	45.1	338	11	Q8CDY4	Q8CDY4 mus musculu
18	761	45.1	304	11	Q91WW5	Q91WW5 mus musculu
19	754	44.7	294	11	Q7TN48	Q7TN48 rattus norv
20	739.5	43.8	301	11	Q91ZC6	Q91ZC6 mus musculu
21	729	43.2	302	11	Q91WW3	Q91WW3 mus musculu
22	722.5	42.8	305	11	Q91ZC5	Q91ZC5 mus musculu
23	713	42.2	321	11	Q91ZC0	Q91ZC0 mus musculu
24	703	41.6	338	11	Q91ZC3	Q91ZC3 mus musculu
25	691.5	41.0	313	11	Q91WW2	Q91WW2 mus musculu
26	681.5	40.4	323	11	Q7TN45	Q7TN45 rattus norv
27	680.5	40.3	305	11	Q91WW4	Q91WW4 mus musculu
28	680	40.3	287	11	Q91ZC7	Q91ZC7 mus musculu
29	674	39.9	322	11	Q91ZB9	Q91ZB9 mus musculu
30	669.5	39.7	305	11	Q91ZC4	Q91ZC4 mus musculu
31	638	37.8	314	11	Q7TN47	Q7TN47 rattus norv
32	626	37.1	353	11	Q7TN44	Q7TN44 rattus norv
33	617.5	36.6	312	11	Q91ZC1	Q91ZC1 mus musculu
34	596.5	35.3	328	11	Q7TN50	Q7TN50 rattus norv
35	578.5	34.3	245	11	Q7TN43	Q7TN43 rattus norv
36	576.5	34.2	247	11	Q7TN46	Q7TN46 rattus norv
37	568.5	33.7	330	11	Q7TN51	Q7TN51 mus musculu
38	506	30.0	321	4	Q8TDS7	Q8TDS7 homo sapien
39	506	30.0	347	4	Q8NGK7	Q8NGK7 homo sapien
40	503	29.8	310	11	Q91ZB7	Q91ZB7 mus musculu
41	489	29.0	321	11	Q91ZB8	Q91ZB8 mus musculu
42	474	28.1	319	11	Q7TN41	Q7TN41 rattus norv
43	464	27.5	309	11	Q7TN40	Q7TN40 rattus norv
44	452.5	26.8	324	11	Q8BH18	Q8BH18 mus musculu
45	448.5	26.6	324	11	Q9D5Q2	Q9D5Q2 mus musculu

ALIGNMENTS

RESULT 1

Q96LB0 PRELIMINARY; PRT; 322 AA.
ID Q96LB0
AC Q96LB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor.
GN MRG33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylika M.J., Simon M.I., Anderson D.J.;
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons."
RL Cell 106:619-632(2001).
DR EMBL; AY042215; AAK91806.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00282; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36484 MW; 253B1BFF0CB4EB74 CRC64;

Query Match 100.0%; Score 1688; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-141;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDSTIPVLGTELPINGRETPCYKQTLSTGTCTIVSLVLTGNVAVLWLLCRRNA 60
|||||

Db 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGTCTCVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300
Db 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322
RESULT 2
Q8TDE1 PRELIMINARY; PRT; 322 AA.
ID Q8TDE1
AC Q8TDE1
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE G protein-coupled receptor SNSR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
Dray A., Walker P., Ahmad S.,
RT "Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474987; AAL86878.2; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36465 MW; 6462C5044F91EA50 CRC64;

Query Match 99.2%; Score 1675; DB 4; Length 322;
Best Local Similarity 99.1%; Pred. No. 2.8e-140;
Matches 319; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGTCTCVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGTCTCVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300
Db 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322
RESULT 3
Q8TDE0 PRELIMINARY; PRT; 322 AA.
ID Q8TDE0
AC Q8TDE0
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE G protein-coupled receptor SNSR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
Dray A., Walker P., Ahmad S.,
RT "Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474988; AAL86879.2; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36594 MW; D8C24308B3B4611B CRC64;
Query Match 95.1%; Score 1606; DB 4; Length 322;
Best Local Similarity 96.0%; Pred. No. 3.6e-134;
Matches 309; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGTCTCVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGTCTCVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300
Db 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322
RESULT 4
Q8TDD9 PRELIMINARY; PRT; 322 AA.
ID Q8TDD9
AC Q8TDD9
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE G protein-coupled receptor SNSR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Barville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474989; AAL86880.2; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36287 MW; 4C43E33E52DCBFF5 CRC64;

Query Match      83.6%; Score 1411; DB 4; Length 322;
Best Local Similarity 84.5%; Pred. No. 6,6e-117;
Matches 272; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCIVSLVLTGNVAVLLGCRMRNA 60
Db 1 MDPTVSTLDTLTPINGTEETLCYKQTLSTGLTCIVSLVLTGNVAVLLGCRMRNA 60

QY 61 VSIYILNVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPIGLSMLSAISTER 120
Db 61 FSIYILNVAADFLFSGRLIYLSLFSIPHTISKILYPMWFSYFAGLSFLSAVSTER 120

QY 121 CLSLWPIWYHCHRRPYLSSVMCVLLWALSRLSILEWFCDFLPSGADSVWCSTSDFIT 180
Db 121 CLSLWPIWYHCHRRPYLSSVMCVLLWALSRLSILEWFCDFLPSGADSVWCSTSDFIT 180

QY 181 IAWLFLCVVLCGSSVLVRLTLCGRKMPRLVTVTLTVLFLCGLPFGIQWALFS 240
Db 181 VAWLFLCVVLCGSSVLVRLTLCGRKMPRLVTVTLTVLFLCGLPFGIQWALFS 240

QY 241 RIHLDKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRQRNQLKLVLQALQDTP 300
Db 241 RIHLDKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRQRNQLKLVLQALQDTP 300

QY 301 VDEGGGWLPOETLELSGRLEQ 322
Db 301 VDEGGGWLPOETLELSGRLEQ 322

RESULT 5
Q96LB2 PRELIMINARY; PRT; 322 AA.
ID Q96LB2
AC Q96LB2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor (Seven transmembrane helix receptor).
GN MRGXI OR GPCR
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21435806; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RA "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons.";
RL Cell 106:619-632(2001).
[2]
RN SEQUENCE FROM N.A.
RX Takeda S., Kadowaki S., Haga T., Takasasu H., Mitaku S.;
RA "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RX Suwa M., Sato T., Okouchi I., Azita M., Furami K., Matsumoto S.,
RA Tautumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
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RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AX042213; AAK91804.1; -.
DR EMBL; AB083628; BAB89341.1; -.
DR EMBL; AB065846; BAC06064.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 322 AA; 36250 MW; C7F3A9F4418E8AD1 CRC64;

Query Match      81.9%; Score 1383; DB 4; Length 322;
Best Local Similarity 83.5%; Pred. No. 2e-114;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCIVSLVLTGNVAVLLGCRMRNA 60
Db 1 MDPTISTLDTLTPINGTEETLCYKQTLSTGLTCIVSLVLTGNVAVLLGCRMRNA 60

QY 61 VSIYILNVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPIGLSMLSAISTER 120
Db 61 FSIYILNVAADFLFSGRLIYLSLFSIPHTISKILYPMWFSYFAGLSFLSAVSTER 120

QY 121 CLSLWPIWYHCHRRPYLSSVMCVLLWALSRLSILEWFCDFLPSGADSVWCSTSDFIT 180
Db 121 CLSLWPIWYHCHRRPYLSSVMCVLLWALSRLSILEWFCDFLPSGADSVWCSTSDFIT 180

QY 181 IAWLFLCVVLCGSSVLVRLTLCGRKMPRLVTVTLTVLFLCGLPFGIQWALFS 240
Db 181 VAWLFLCVVLCGSSVLVRLTLCGRKMPRLVTVTLTVLFLCGLPFGIQWALFS 240

QY 241 RIHLDKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRQRNQLKLVLQALQDTP 300
Db 241 RIHLDKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRQRNQLKLVLQALQDTP 300

QY 301 VDEGGGWLPOETLELSGRLEQ 322
Db 301 VDEGGGWLPOETLELSGRLEQ 322

RESULT 6
Q8TDD7 PRELIMINARY; PRT; 322 AA.
ID Q8TDD7
AC Q8TDD7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor SNRS5.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Barville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474989; AAL86880.2; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
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DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 322 AA; 36423 MW; 3D6FFB4B5DDFD90 CRC64;

Query Match
Best Local Similarity 81.9%; Score 1382; DB 4; Length 322;
Matches 268; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
DB 1 MDPTVPVLGKLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILMPIWHCHRRPRYLSSVMCVLLWALSLSILEWMFCDFLFGADSVMCETSDFIT 180
DB 121 CLSILMPIWHCHRRPRYLSSVMCVLLWALSLSILEWMFCDFLFGADSVMCETSDFIT 180
QY 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLTRLYVTILLTVLFLCGLPFGIQWALFS 240
DB 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLTRLYVTILLTVLFLCGLPFGIQWALFS 240
QY 241 RIHLWKVLFCHVHLVIFLSALNSSANPIYFFVGSFRQNRQNLKLVQALQDTP 300
DB 241 RIHLWKVLFCHVHLVIFLSALNSSANPIYFFVGSFRQNRQNLKLVQALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 8
Q96LA9 PRELIMINARY; PRT; 322 AA.
AC Q96LA9
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE G protein-coupled receptor.
GN MRGX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36434 MW; 7CA676F8BD390A31 CRC64;

Query Match
Best Local Similarity 81.0%; Score 1367; DB 4; Length 322;
Matches 266; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
DB 1 MDPTVPVLGKLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPIKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILMPIWHCHRRPRYLSSVMCVLLWALSLSILEWMFCDFLFGADSVMCETSDFIT 180
DB 121 CLSILMPIWHCHRRPRYLSSVMCVLLWALSLSILEWMFCDFLFGADSVMCETSDFIT 180
QY 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLTRLYVTILLTVLFLCGLPFGIQWALFS 240
DB 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLTRLYVTILLTVLFLCGLPFGIQWALFS 240
QY 241 RIHLWKVLFCHVHLVIFLSALNSSANPIYFFVGSFRQNRQNLKLVQALQDTP 300
DB 241 RIHLWKVLFCHVHLVIFLSALNSSANPIYFFVGSFRQNRQNLKLVQALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 7
Q8TDD8 PRELIMINARY; PRT; 322 AA.
AC Q8TDD8
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE G protein-coupled receptor SNR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lenbo B.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hofert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209 (2002).
DR EMBL: AF474990; AAJ86881.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36236 MW; C301BC174BB01D72 CRC64;

Query Match
Best Local Similarity 81.9%; Score 1382; DB 4; Length 322;
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QY 121 CLSLWPIWYHCRPRRYLSSVNCVLLWALSILRSILEMFCDFLFSGADSVWCETSDFIT 180
D 121 CLSLWPIWYHCRPRRYLSSVNCVLLWALSILRSILEMFCDFLFSGADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSLVLLVRLICGRKMPRLTRLYVTILLTVLVFLCGLPFGIOWALFS 240
D 181 VAWLIFLCVLCVSSVLVLLVRLICGRKMPRLTRLYVTILLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKLVLRALQDTPE 300
D 241 RMHLNLEVLVCHVYLVCMSSLSNNSANPIIYFFVGSFRQRNQNLKLVLRALQDKPE 300
QY 301 VDEGGGWLPOETLELSGSR 320
D 301 VDKGSQLPEESLELSGSR 320
RESULT 9
Q8TDD6 PRELIMINARY; PRT; 322 AA.
AC Q8TDD6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor SNR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCR."
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474992; AAL86883.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW SEQUENCE 322 AA; 36434 MW; 7CA66E58D70548BA CRC64;
Query Match 80.6%; Score 1360; DB 4; Length 322;
Best Local Similarity 82.5%; Pred. No. 2.2e-112;
Matches 264; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 1 MDSTPVLGTETPTNGRETCYQTLSTGLTCTIVSLVLTGNVAVLWLLGCRNRNA 60
D 1 MDPTVPTVGTETPTNGRETCYQTLSTGLTCTIVSLVLTGNVAVLWLLGCRNRNA 60
QY 61 VSIYILNVAADFLVLSGHIICSPRLINIRIPISKILSPVNTFFYFGLSMLSAISTER 120
D 61 VSIYILNVAADFLVLSGHIICSPRLINIRIPISKILSPVNTFFYFGLSMLSAISTER 120
QY 121 CLSLWPIWYHCRPRRYLSSVNCVLLWALSILRSILEMFCDFLFSGADSVWCETSDFIT 180
D 121 CLSLWPIWYHCRPRRYLSSVNCVLLWALSILRSILEMFCDFLFSGADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSLVLLVRLICGRKMPRLTRLYVTILLTVLVFLCGLPFGIOWALFS 240
D 181 VAWLIFLCVLCVSSVLVLLVRLICGRKMPRLTRLYVTILLTVLVFLCGLPFGIOWALFS 240
QY 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRNQNLKLVLRALQDTPE 300
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Db 241 RMHLNLEVLVCHVYLVCMSSLSNNSANPIIYFFVGSFRQRNQNLKLVLRALQDKPE 300
QY 301 VDEGGGWLPOETLELSGSR 320
D 301 VDKGSQLPEESLELSGSR 320
RESULT 10
Q96LB1 PRELIMINARY; PRT; 330 AA.
AC Q96LB1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor (Seven transmembrane helix receptor).
GN MRG2 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RA "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons."
RL Cell 106:619-632(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tutsuni S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY042214; AAK91805.1; -.
DR EMBL; AB083626; BAB89339.1; -.
DR EMBL; AB065811; BAC06030.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor; Transmembrane.
KW SEQUENCE 330 AA; 37099 MW; CB38FD78B1DF6BE CRC64;
Query Match 58.6%; Score 989.5; DB 4; Length 330;
Best Local Similarity 62.1%; Pred. No. 1.4e-79;
Matches 208; Conservative 27; Mismatches 79; Indels 21; Gaps 5;
QY 1 MDSTPVLGTETPTNGRETCYQTLSTGLTCTIVSLVLTGNVAVLWLLGCRMR 57
D 1 MDPTPANGTESITVNGDQALLLCKETLIPVFLIFLIALVGLVNGFVLLGFRMR 60
QY 58 RNAVSIVILNVAADFLVLSGHIICSPRLINIRIPISKILSPVNTFFYF 107
D 61 RNAFSVTVLSAGADFLVLCFQINCLVLSNFCFSCSISINFP--SEFTVTMCAYL 114
QY 108 IGLSMLSAISTERCLSLWPIWYHCRPRRYLSSVNCVLLWALSILRSILEMFCDFLFSG 167
D 115 AGLSMLSTVSTERCLSVLWPIWYHCRPRRYLSSVNCVLLWALSILRSILEMFCDFLFSG 174
QY 168 ADSVWCETSDFITIANLVFLCVLGGSLVLLVRLICGRKMPRLTRLYVTILLTVLVFL 227
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Db 175 GSGWCQTDFITAAWLIFFLFWLVCSSALLVRLCGSRGLPLRLYLTLTLVLFLL 234
Qy 228 CGLPFGIOWALFSRIHLDNKKVLFCHVHVSIFLSALNSSANPIIYFFVGSFRQRNQ- 286
Db 235 CGLPFGIOWFLILWIKDSDVLFCHVHVSIVLSSANPIIYFFVGSFRKQRLQOP 294
Qy 287 -LKLVLQRALQDTPEVDEGGWLPQETLSSGRL 320
Db 295 ILKALQRALQDIAEVDHSGCFRQGTPEMSRSL 329

RESULT 11
Q7TN42 PRELIMINARY; PRT; 323 AA.
AC Q7TN42;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE MRGC G protein-coupled receptor.
GN MRGC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22810130; PubMed=12909716;
RA Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT "Atypical expansion in mice of the sensory neuron-specific Mrg G
protein-coupled receptor family."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048 (2003).
DR EMBL; AF518245; AAQ08317.1; -.
KW Receptor.
SQ SEQUENCE 323 AA; 50639FDAE42E8052 CRC64;

Query Match 48.8%; Score 823.5; DB 11; Length 323;
Best Local Similarity 52.8%; Pred. No. 6.7e-65;
Matches 172; Conservative 51; Mismatches 92; Indels 11; Gaps 6;
Qy 1 MDSTIPVLGTLPINGRETPCYKQTLSTGTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDPTISLSTESTLNKTGHPSC-RPILTLFSLVPIITLLAGNTIVLWLLGFRMRKA 59
Qy 61 VSYILNLVAADFELSGHICSPRLINI----RHPISK-ILSPVMTFFYFGLSMLSA 115
Db 60 ISVYVNLNLSDSFFLCCHFDLSLRIMNFIYAHKLSKEILGNVAFIPYISGLSLSA 119
Qy 116 ISTERCLSIILWPIWYHCHRRPRYSVVMCVLLWALSLSLRILEWMCDFLPSGADSVWCET 175
Db 120 ISTERCLSVLWPIWYHCHRRPRNSAICVLIVLWLSFLMGILDWFFSGFLGETHHLLW-KN 178
Qy 176 SDFITIAWLVLCVLCGSSLVLLVRLCGSRKMPRLYVTLTLVFLVLCGLPFGIQ 235
Db 179 VDFIVTAFILFLFWLLFGSSALLVRLCGSRKPLSRLYVTISLVVWVLLICGLPLGY 238
Qy 236 WAL--FSRIHLDNKKVLFCHVHVSIFLSALNSSANPIIYFFVGSFRQRNQRLKVLQR 293
Db 239 LFLYWFGLHLYP--FCHIVQVTVLLSCVNSSANPIIYFVGSFRHKKHRSKMLVKR 296
Qy 294 ALQDTPVDEGGWLPQETLSSGSR 319
Db 297 ALBETPEDEYTDHVKQKTEISERR 322

RESULT 12
Q8R4G1 PRELIMINARY; PRT; 337 AA.
AC Q8R4G1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE MRGC G protein-coupled receptor.
GN MRGC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22810130; PubMed=12909716;
RA Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT "Atypical expansion in mice of the sensory neuron-specific Mrg G
protein-coupled receptor family."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048 (2003).
DR EMBL; AF518245; AAQ08317.1; -.
KW Receptor.
SQ SEQUENCE 337 AA; 50639FDAE42E8052 CRC64;

Query Match 48.6%; Score 820.5; DB 11; Length 337;
Best Local Similarity 52.5%; Pred. No. 1.3e-64;
Matches 171; Conservative 51; Mismatches 93; Indels 11; Gaps 6;
Qy 1 MDSTIPVLGTLPINGRETPCYKQTLSTGTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 15 MDPTISLSTESTLNKTGHPSC-RPILTLFSLVPIITLLAGNTIVLWLLGFRMRKA 73
Qy 61 VSYILNLVAADFELSGHICSPRLINI----RHPISK-ILSPVMTFFYFGLSMLSA 115
Db 74 ISVYVNLNLSDSFFLCCHFDLSLRIMNFIYAHKLSKEILGNVAFIPYISGLSLSA 133
Qy 116 ISTERCLSIILWPIWYHCHRRPRYSVVMCVLLWALSLSLRILEWMCDFLPSGADSVWCET 175
Db 134 ISTERCLSVLWPIWYHCHRRPRNSAICVLIVLWLSFLMGILDWFFSGFLGETHHLLW-KN 192
Qy 176 SDFITIAWLVLCVLCGSSLVLLVRLCGSRKMPRLYVTLTLVFLVLCGLPFGIQ 235
Db 193 VDFIVTAFILFLFWLLFGSSALLVRLCGSRKPLSRLYVTISLVVWVLLICGLPLGY 252
Qy 236 WAL--FSRIHLDNKKVLFCHVHVSIFLSALNSSANPIIYFFVGSFRQRNQRLKVLQR 293
Db 253 LFLYWFGLHLYP--FCHIVQVTVLLSCVNSSANPIIYFVGSFRHKKHRSKMLVKR 310
Qy 294 ALQDTPVDEGGWLPQETLSSGSR 319
Db 311 ALBETPEDEYTDHVKQKTEISERR 336

RESULT 13
Q8CIP3 PRELIMINARY; PRT; 322 AA.
AC Q8CIP3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor MrgC11.
GN MRGC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22317401; PubMed=12397184;
RA Han S.K., Dong X., Hwang J.I., Zylka M.J., Anderson D.J., Simon M.I.;
RT "Orphan G protein-coupled receptors MrgA1 and MrgC11 are distinctively
activated by RF-amide-related peptides through the Galpha q/11
pathway."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14740-14745 (2002).
DR EMBL; AY152435; AAN64385.1; -.
KW GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
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DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007185; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36809 MW; 1E03ECD544AF86DC CRC64;

Query Match 47.2%; Score 797; DB 11; Length 322;
Best Local Similarity 53.2%; Pred. No. 1.5e-62;
Matches 174; Conservative 43; Mismatches 96; Indels 14; Gaps 8;

QY 1 MDSTIPVLGTLPINGREETPCYK-QTLSFTGLTCIVSLVALTGNVVLWLLGCRMRN 59
DB 1 MDPTSSHDTESTPNETGHPNCTPILTLP--LVLTITVLGLAGNTVLWLLGFRMRK 58

QY 60 AVSIYILNLVAADFLSLGHIICSPRLINIRP----RHPISK-ILSPVMTFFYFGLSMLS 114
DB 59 AISVILNLALADSFLLCHFDLSLRIDFYGLVAHKLSDILGNAAIIFYISGLSILS 118

QY 115 AISTERCILWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVWCE 174
DB 119 AISTERCILWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVW 176

QY 175 TDSFTITIAWLVFLVCVLCSSLVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPGL 234
DB 177 NVDFITIAFLFLFLLGSSLLALLRLICGPRKPLSLRYVTIALTVWVLIICGLPGL 236

QY 235 QWAL--FSRIHLDWKVLFCHVHLSIFLSALNSSANPIIYFVSGFRQRQNRQNLKVLQ 292
DB 237 YLFLLYFVGHLYHP--FCHYQVAVLSVNCSSANPIIYFVSGFRQRKHSRLKVLK 294

QY 293 RALQDTPEVDEGGWLPQETLELSGSR 319
DB 295 RALQDTPEVDEYTDHSLHKTTSISGR 321

RESULT 14
Q7TN49
ID Q7TN49 PRELIMINARY; PRT; 304 AA.
AC Q7TN49;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRGA G protein-coupled receptor.
GN MRGA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RT "Cloning and functional characterization of the rat orphan GPCR
RT rc 56.1.3."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311952; CAC84592.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor.
SQ SEQUENCE 331 AA; 37005 MW; 74BAEA8C557859AC CRC64;

Query Match 46.1%; Score 778; DB 11; Length 331;
Best Local Similarity 53.3%; Pred. No. 7.3e-61;
Matches 176; Conservative 33; Mismatches 85; Indels 36; Gaps 8;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVS-LVALTGNVVLWLLGCRMRN 59
DB 28 MDXTIP-----GSFNRTLP-----NLLIISGLVGLIGNAVWVLLGFLARN 72

QY 60 AVSIYILNLVAADFLSLGHIICSPRLINIRP----ISKILSPVMTFFYFGLSMLS 116
DB 73 AFSVILNLALADFLFLCHIIDSTLLLKFSYPNIIFPCFNTVMVPIYIAGLSMLS 132

QY 117 STERCILWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVW---- 172
DB 133 STERCILWVCPWYRCRRPKHTSTVMCSAIWVLSLLICILNRYFCGFL----DTKYEKDN 188

QY 173 -CETSDFTITIAWLVFLVCVLCSSLVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLP 231
DB 189 RCLASNEFTAACLIFFLVLCSSLLALLVRLFCGAGMKLTRLYATIMLTIVLVLGCLP 248
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Qy	232	FGIOWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNKLV	291
Db	249	FGIHWFLIIWIKIDYGFAYGLVLAALVLTAVNSCANPIIYFFVGSFR-HQKHQTLKMW	307
Qy	292	ORALQDTPVEDEGGWLPQETLELSGRLE	321
Db	308	ORALQDTPETAETAE-----NTVEMSSSKVE	330

Search completed: July 4, 2004, 08:45:29
Job time : 73 secs

GenCore version 5.1.6
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Run on: July 4, 2004, 04:48:57 ; Search time 4166 Seconds
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Title: US-09-787-879C-3
Perfect score: 969
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 1: gb.ba.*
- 2: gb.htg.*
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- 11: gb.sts.*
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- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
1	969	100.0	969	6	E43450	E43450 Novel prote
2	969	100.0	969	6	AX498196	AX498196 Sequence
3	969	100.0	1400	6	AX299158	AX299158 Sequence
4	969	100.0	1400	6	AX549388	AX549388 Sequence
5	969	100.0	1400	9	AY042215	AY042215 Homo sapi
6	969	100.0	2618	6	AX429465	AX429465 Sequence
7	969	100.0	8622	6	AX429467	AX429467 Sequence
8	967.4	99.8	969	6	E43451	E43451 Novel prote
C 9	967.4	99.8	91923	9	AC108007	AC108007 Homo sapi
10	965.8	99.7	969	6	AX923125	AX923125 Sequence
11	965.8	99.7	1388	6	AX647081	AX647081 Sequence
C 12	965.8	99.7	172939	9	AC090099	AC090099 Homo sapi
13	961	99.2	969	9	AF474987	AF474987 Homo sapi
14	949.8	98.0	969	6	BD103571	BD103571 Novel G p
15	945	97.5	969	9	AF474988	AF474988 Homo sapi
16	938.6	96.9	969	6	BD103572	BD103572 Novel G p
17	837.8	86.5	969	6	E40003	E40003 Novel G pro
18	837.8	86.5	969	9	AF474989	AF474989 Homo sapi
C 19	837.8	86.5	156839	9	AC107948	AC107948 Homo sapi
20	836.2	86.3	969	6	BD103575	BD103575 Novel G p
21	836.2	86.3	969	9	AF474991	AF474991 Homo sapi
22	834.6	86.1	969	6	E40000	E40000 Novel G pro
23	833	86.0	969	6	E39999	E39999 Novel G pro
24	833	86.0	969	6	AX498194	AX498194 Sequence
25	833	86.0	969	6	BD103573	BD103573 Novel G p
26	833	86.0	1389	6	AX646849	AX646849 Sequence
27	833	86.0	1604	6	AX299160	AX299160 Sequence
28	833	86.0	1604	6	AX549403	AX549403 Sequence
29	833	86.0	1604	9	AY042216	AY042216 Homo sapi
30	831.4	85.8	969	9	AF474992	AF474992 Homo sapi
31	829.8	85.6	969	6	AX148178	AX148178 Sequence
32	829.8	85.6	969	6	AX268489	AX268489 Sequence
33	829.8	85.6	969	6	AX375428	AX375428 Sequence
34	829.8	85.6	969	6	AX671113	AX671113 Sequence
35	829.8	85.6	969	6	BD103576	BD103576 Novel G p
36	829.8	85.6	969	6	BD144297	BD144297 Novel G-p
37	829.8	85.6	969	9	AB083628	AB083628 Homo sapi
38	829.8	85.6	969	9	AF474990	AF474990 Homo sapi
39	829.8	85.6	969	6	AX921831	AX921831 Sequence
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C 45	829.8	85.6	165490	2	AC139482	AC139482 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS E43450 Novel protein G-coupled receptor protein and DNA thereof. 969 bp DNA linear PAT 31-JAN-2002
DEFINITION E43450
ACCESSION E43450
VERSION E43450.1 GI:18627716
KEYWORDS JP 2000166576-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS Watanabe,T., Terao,S. and Matsui,H.
TITLE Novel protein G-coupled receptor protein and DNA thereof
JOURNAL Patent: Jp 2000166576-A 1 20-JUN-2000;

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COMMENT
OS Homo sapiens (human)
PN JP 2000166576-A/1
PD 20-JUN-2000
PF 30-SEP-1999 JP 1999278116
PR TAKUYA WATANABE,SHIZUKO TERAU,HIDEKI MATSUI
PC C12N15/09,A61K39/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P43/00,
PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,C12P21/08,PC
GOIN33/15,
PC
GOIN33/53,GOIN33/566,GOIN33/577/(C12N1/21,C12R1:19),(C12N5/10,PC
C12R1:91),
PC (C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,A61K37/02,
PC C12N5/00,
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ORIGIN
Query Match 100.0%; Score 969; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 1e-244;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTCAACCATCCAGCTCTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG 60
DB 1 ATGATTCAACCATCCAGCTCTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG 60
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DB 61 ACTCTTGTCTACAGCAGACCTGAGCTTCAAGGCTGACGTGCTGCTTCCCTTGTCT 120
QY 121 GCGGTGACAGAAACGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 GCGGTGACAGAAACGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 121 GCGGTGACAGAAACGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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DB 241 ATATGTTGCGCGTTACCGCTCATCAATATCGCGCTGACGAGCTGTACGATTCCTCT 300
QY 301 GTGATGACCTTTCCTACTTATAGGCTTAAGCATGCTGAGCGGCATCAGCACCAGCGC 360
DB 301 GTGATGACCTTTCCTACTTATAGGCTTAAGCATGCTGAGCGGCATCAGCACCAGCGC 360
QY 361 TGCTGTCCATCTCTGTGCGCCATCTGTGTAACATGCGCGCCGCGCCAGATACCTGTATCG 420
DB 361 TGCTGTCCATCTCTGTGCGCCATCTGTGTAACATGCGCGCCGCGCCAGATACCTGTATCG 420
QY 421 GTCATGTGTCTGCTGCTGCGCCCTGTCCCTGCTGCGGAGTATCTCTGAGTGTGATGTC 480
DB 421 GTCATGTGTCTGCTGCTGCGCCCTGTCCCTGCTGCGGAGTATCTCTGAGTGTGATGTC 480
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DB 481 TGTGATCTCTCTGTGTGTGCTGATCTGTTTGTGTGTAACGTCAGATTCATTAACA 540
QY 541 ATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 ATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AGGATTTCTGTGGATCCCGGAAGATGCCGTGACGAGCTGTACGTGACATCTCTCTCT 660
DB 601 AGGATTTCTGTGGATCCCGGAAGATGCCGTGACGAGCTGTACGTGACATCTCTCTCT 660

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QY 841 CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTCGACGACACGCGCTGAG 900
Db 1172 CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTCGACGACACGCGCTGAG 1231
QY 901 GTGGATGAAGGTGGAGGTGGCTTCTCTCAGGAACCCCTGGAGCTCTCGGAGACAGATTG 960
Db 1232 GTGGATGAAGGTGGAGGTGGCTTCTCTCAGGAACCCCTGGAGCTCTCGGAGACAGATTG 1291
QY 961 GAGCAGTGA 969
Db 1292 GAGCAGTGA 1300

RESULT 4
AX549388 1400 bp DNA linear PAT 26-NOV-2002
LOCUS AX549388
DEFINITION Sequence 673 from Patent WO02061087.
ACCESSION AX549388
VERSION AX549388.1 GI:25814004
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Burner G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 673 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
source
1. .1400
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 969; DB 6; Length 1400;
Best Local Similarity 100.0%; Pred. No. 1.1e-244;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG 60
Db 332 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG 391
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DEFINITION Homo sapiens G protein-coupled receptor (MRGX3) gene, complete cds.
ACCESSION AX042215
VERSION AX042215.1 GI:15546055
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Dong, X., Han, S., Zylka, M.J., Simon, M.I. and Anderson, D.J.
TITLE A diverse family of GPCRs expressed in specific subsets of
nociceptive sensory neurons
JOURNAL Cell 106 (5), 619-632 (2001)
MEDLINE 21435808
PubMed 11551509
REFERENCE
AUTHORS Dong, X., Han, S.K., Zylka, M.J., Simon, M.I. and Anderson, D.J.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2001) Division of Biology, 216-76, California
Institute of Technology, 1201 E. California Blvd., Pasadena, CA
91125, USA
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VERSION AX429465.1 GI:21540763
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhao,Q., Beasley,E.M. and Wei,M.H.
TITLE Isolated human g-protein coupled receptors, nucleic acid molecules
encoding human gpr proteins, and uses thereof
JOURNAL Patent: WO 0234914-A 1 02-MAY-2002;
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Qy 241 ATATGTTGCGCGTTAGCCCTCATATCCGCCATCCCATCTCGAAATCTCAGTCCT 300
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 969)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Watanabe, T., Texao, S. and Matsui, H.
Novel protein G-coupled receptor protein and DNA thereof
Patent: JP 2000166576-A 2 20-JUN-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
FN JP 2000166576-A/2
PD 20-JUN-2000
PF 30-SEP-1999 JP 1999278116
PR
PI TAKUYA WATANABE, SHIZUKO TERAOKA, HIDEKI MATSUI
PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61K48/00,
PC A61P43/00,
PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/02, C12P21/08, PC
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ORIGIN
Query Match 99.8%; Score 967.4; DB 6; Length 969;
Best Local Similarity 99.9%; Pred. No. 2.7e-244;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTTGAGGAG 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 91923)
Homo sapiens chromosome 11, clone CTD-3038L12, complete sequence.
AUTHORS
Birren, B., Nusbaum, C. and Lander, E.
TITLE
Homo sapiens chromosome 11, clone CTD-3038L12
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 91923)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguski, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choquel, Y., Collangelo, M., Collins, S., Collumore, A., Cook, A.,
Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
Farrisa, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Gande, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C.,
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Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome


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REFERENCE
AUTHORS
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  3 (bases 1 to 91923)
  Birren,B., Nushbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
  Barina,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
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  Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
  Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
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  Zembek,L., Zimmer,A. and Zody,M.
  Direct Submission
  Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  4 (bases 1 to 91923)
  Birren,B., Nushbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
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  Zembek,L., Zimmer,A. and Zody,M.
  Direct Submission
  Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome
  Research, 320 Charles Street, Cambridge, MA 02141, USA
  On Sep 3, 2002 this sequence version replaced GI:22474954.
  All repeats were identified using RepeatMasker:
  Smit, A.F.A. & Green, P. (1996-1997)
  http://ftp.genome.washington.edu/RM/RepeatMasker.html
  ----- Genome Center
  Center: Whitehead Institute/ MIT Center for Genome Research
  Center code: WIBR
  Web site: http://www-seq.wi.mit.edu
  Contact: sequence_submissions@genome.wi.mit.edu
  ----- Project Information
  Center project name: L24596
  Center clone name: 3038_L12
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  Only the first 91.9 kb of this clone are being submitted.
  The remainder overlaps accession number AC055860 [WICGR project
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Query Match 99.8%; Score 967.4; DB 9; Length 91923;
Best Local Similarity 99.9%; Pred. No. 6.8e-244;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 9477 ATGGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAACGAGTGAAGAG 9418

QY 61 ACTCCTTGCTACAGACACCTGAGCTTCAAGGGGCTGACGTGCAATGCTTCCCTTGTG 120
DB 9417 ACTCCTTGCTACAGACACCTGAGCTTCAAGGGGCTGACGTGCAATGCTTCCCTTGTG 9358

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DB 9357 GCCTGACAGAAACGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9298

QY 181 GTCTCCATACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 9297 GTCTCCATACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9238

QY 241 ATATGTTGGCGTTACGCTATCAATATCGGCAATCCATCTCCAAATCTCAGTCTCT 300
DB 9237 ATATGTTGGCGTTACGCTATCAATATCGGCAATCCATCTCCAAATCTCAGTCTCT 9178

QY 301 GTGATGACCTTTCCTACTTATAGGCTTAAGATGCTGAGCGCATCAGACCGAGCGC 360
DB 9177 GTGATGACCTTTCCTACTTATAGGCTTAAGATGCTGAGCGCATCAGACCGAGCGC 9118

QY 361 TGCCTGTCATCTGTGGCCATCTGTACACCTGCGCGCGCCCGCCAGATACCTGTGATCG 420
DB 9117 TGCCTGTCATCTGTGGCCATCTGTACACCTGCGCGCGCCCGCCAGATACCTGTGATCG 9058

QY 421 GTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 9057 GTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8998

QY 481 TGTGACTTCCTGTTTGTGTTGCTGATCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 540
DB 8997 TGTGACTTCCTGTTTGTGTTGCTGATCTGTTTGTGTTGTTGTTGTTGTTGTTGTT 8938

QY 541 ATCCGCTGGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
DB 8937 ATCCGCTGGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 8878

QY 601 AGGATTCCTGCTGATCCCGAAGATCCGCTGACCAAGGTGTACGTGACCACTCCTCCTC 660
DB 8877 AGGATTCCTGCTGATCCCGAAGATCCGCTGACCAAGGTGTACGTGACCACTCCTCCTC 8818

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DB 8817 ACAGTGTGCTTCTCCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8758

QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTGTGATGCTGATGCTGATGCTGATGCTGCT 780
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QY 781 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCTGGGGCTCTTTAGGCAG 840
DB 8697 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCTGGGGCTCTTTAGGCAG 8638

QY 841 CGTCAAAATAGGCAGAACCTGAAAGTGGTCTTCAGAGGGCTCTGAGGACACCCCTGAG 900
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QY 901 GTGGATGAAGGTGAGGGTGGCTTCTTCAGAAACCTTGGAGCTGTGGGAGCAGATTG 960
DB 8577 GTGGATGAAGGTGAGGGTGGCTTCTTCAGAAACCTTGGAGCTGTGGGAGCAGATTG 8518

QY 961 GAGCAGTGA 969
DB 8517 GAGCAGTGA 8509

RESULT 10
AX923125
LOCUS AX923125
DEFINITION Sequence 1 from Patent WO03080659.
ACCESSION AX923125
VERSION AX923125.1 GI:40216228
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Peri, K.G., Moffett S. and Abtan, D.
TITLE Methods and compounds for prevention and treatment of elevated intraocular pressure and related conditions
JOURNAL Patent: WO 03080659-A 1 02-OCT-2003;
THERATECHNOLOGIES INC. (CA)
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CDS 1..969
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ORIGIN
Query Match 99.7%; Score 965.8; DB 6; Length 969;
Best Local Similarity 99.8%; Pred. No. 7e-244;
Matches 967; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 ACTCCTTGCTACAGACACCTGAGCTTCAAGGGGCTGACGTGCAATGCTTCCCTTGTG 120
DB 61 ACTCCTTGCTACAGACACCTGAGCTTCAAGGGGCTGACGTGCAATGCTTCCCTTGTG 120

QY 121 GCGCTGACAGGAAACCGGTTGTGCTCTGGGCTCTGGGCTGCGCATGCGAGGAACGCT 180
DB 121 GCGCTGACAGGAGACGGGTTGTGCTCTGGGCTCTGGGCTGCGCATGCGAGGAACGCT 180

QY 181 GTCTCCATACATCTCAACCTGCTGCGGCGCACTTCCCTTCTTTAGCGGCCACATT 240
DB 181 GTCTCCATACATCTCAACCTGCTGCGGCGCACTTCCCTTCTTTAGCGGCCACATT 240

QY 241 ATATGTTGGCGTTACGCTATCAATATCGGCAATCCATCTCCAAATCTCAGTCTCT 300

241	DB	ATATGTTGCGCGTTAAGCCTCATCAATATCCGCATCCCATCTCCAAAATCCTAGTCCT	300
301	QY	GTGATGACCTTTCCCTACTTTATAGCCCTAAGATGCTGAGCGCCATCAGACCCGAGCGC	360
301	DB	GTGATGACCTTTCCCTACTTTATAGCCCTAAGCATCTGAGCGCCATCAGACCCGAGCGC	360
361	QY	TGCCTGTCCATCTCTGTGGCCCATCTGTTACCATCGCCCGCCAGATACCTGTATCG	420
361	DB	TGCCTGTCCATCTCTGTGGCCCATCTGTTACCATCGCCCGCCAGATACCTGTATCG	420
421	QY	GTCAATGTGTCTCTCTGGGCCCTGTCCCTGCTGGAGATATCTGAGTGGATGTC	480
421	DB	GTCAATGTGTCTCTCTGGGCCCTGTCCCTGCTGGAGATATCTGAGTGGATGTC	480
481	QY	TGTGACATCTCTGTTTGTAGTGGTGTGATCTCTGTTGGTGTGAACGTCAGATTTCATTACA	540
481	DB	TGTGACATCTCTGTTTGTAGTGGTGTGATCTCTGTTGGTGTGAACGTCAGATTTCATTACA	540
541	QY	ATCGCGTGGCTGTTTTTTTATGTGTGGTGTCTCTGTGGTTCAGACCTGTCTGCTGGTGC	600
541	DB	ATCGCGTGGCTGTTTTTTTATGTGTGGTGTCTCTGTGGTTCAGACCTGTCTGCTGGTGC	600
601	QY	AGGATTCTCTGTGGATCCCGAAGATCCCGTACACAGGCTGTACCTGACCATCTCTCTCTC	660
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661	DB	ACAGTGTGTGCTCTCTCTCTGTGGCTCTGCTGGTGGATTCAGTGGGCCCTGTTTTC	720
721	QY	AGGATCCACCTGGATTGGAAGTCTTATTTGTTCATGTGCATCTAGTTTCCATTTCCTTG	780
721	DB	AGGATCCACCTGGATTGGAAGTCTTATTTGTTCATGTGCATCTAGTTTCCATTTCCTTG	780
781	QY	TCGCTCTTAACAGCAGTGCACACCCATCAATTCTCTCTGGGGCTCTTTTAGCGAG	840
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841	QY	CGTCAAAATAGCAGAACCTCAAGCTGGTCTCCAGAGGCTCTGAGAGACACGCTGAG	900
841	DB	CGTCAAAATAGCAGAACCTCAAGCTGGTCTCCAGAGGCTCTGAGAGACACGCTGAG	900
901	QY	GTGGATGAAGTGGAGGTGCTTCTCAGAAAACCTGGAGCTGTGGGAACAGATTG	960
901	DB	GTGGATGAAGTGGAGGTGCTTCTCAGAAAACCTGGAGCTGTGGGAACAGATTG	960
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961	DB	GAGCAGTGA 969	
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LOCUS	AX647081 1369 bp DNA linear PAT 04-MAR-2000		
DEFINITION	Sequence 1273 from Patent EP1270724.		
ACCESSION	AX647081		
VERSION	AX647081.1 GI:28800068		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.		
TITLE	Guanosine triphosphate-binding protein coupled receptors		
JOURNAL	Patent: EP 1270724-A 1273 02-JAN-2003; National Institute of Advanced Industrial Science and Technology (JP) ; Center for Advanced Science and Technology Incubation, Ltd. (JP)		
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source	1..1369 /organism="Homo sapiens"		

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841	CGTCAAAATAGGCAGAACCTTGAAGCTGGTTCTTCAGAGGCTCTGCAGGACACGCCTGAG	900
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Qy		
901	GTGGATCAAGGTGAGAGGTGGCTTCTTCAGGAACCTTGAGCTGTCCGGAACACGATTG	960
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Qy		
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Db		
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RESULT 12	AC090099	172939 bp	DNA linear	PRI 01-OCT-2002
LOCUS	AC090099/c			
LOCUS				
DEFINITION	Homo sapiens chromosome 11, clone RP11-113D6, complete sequence.			
ACCESSION	AC090099			
VERSION	AC090099.14	GI:23396332		
KEYWORDS	HTG.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 172939)			
AUTHORS	Barren,B., Nusbaum,C. and Lander,E.			
TITLE	Homo sapiens chromosome 11, clone RP11-113D6			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 172939)			
AUTHORS	Barren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,			

RESULT 13	AF474987	LOCUS	969 bp	DNA	linear	PRI 16-JUN-2003
DEFINITION	Human sapiens G protein-coupled receptor SNSR1 gene, complete cds.					
ACCESSION	AF474987					
VERSION	AF474987.2	GI:31747894				
KEYWORDS						
SOURCE	Human sapiens (human)					
ORGANISM	Human sapiens					
REFERENCE	1 (bases 1 to 969)					
AUTHORS	Lembo, P.M., Grazzini, E., Groblewski, T., O'Donnell, D., Roy, M.-O., Zhang, J., Hoffert, C., Cao, J., Schmidt, R., Pelletier, M., Labarre, M., Gosselin, M., Fortin, Y., Banville, D., Shen, S., Strom, P., Payza, K., Dray, A., Walker, P., and Ahmad, S.					
TITLE	Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs					
JOURNAL	Nat. Neurosci. 5 (3), 201-209 (2002)					
MEDLINE	21853733					
PUBMED	11850634					
REFERENCE	2 (bases 1 to 969)					
AUTHORS	Ahmad, S., Banville, D., Fortin, Y., Lembo, P.M. and O'Donnell, D.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-JAN-2002) Molecular Biology, Astrazeneca, 7171 Frederick-Banting, Montreal, Quebec H4S 1Z9, Canada					
COMMENT	On Jun 16, 2003 this sequence version replaced gi:19338907.					
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Matches 964;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;		
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Db	61	ACTGCTTGCTCAAGACAGACACCTGAGCTTACGGGGCTGACGTGCATGCTTCCCTTGTC	120			
Qy	121	CGCGTGACAGGAACGCGGTTGTGCTCTGGGCTCTCTGGGCTCCCGCATCGCGAGGAACGCT	180			
Db	121	CGCGTGACAGGAACGCGGTTGTGCTCTGGGCTCTCTGGGCTCCCGCATCGCGAGGAACGCT	180			
Qy	181	GTCCTCACTACCTTCAACCTGGTCCGCGCGCACTTCTCTTCCCTTAGCGGCACATT	240			
Db	181	GTCCTCACTACCTTCAACCTGGTCCGCGCGCACTTCTCTTCTTCTTAGCGGCACATT	240			
Qy	241	ATATGTTCCGGTTACGGCTCATCAATACCGGCATCCCATCTCCAAATCCTCAGTCCCT	300			
Db	241	ATATGTTCCGGTTACGGCTCATCAATACCGGCATCCCATCTCCAAATCCTCAGTCCCT	300			
Qy	301	GTGATGACCTTTCCCTACTTTATTAGCGCTTAAGCATGTGACGGCCATCAGACACCGAGCG	360			

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Strandedness: Double;
CC Topology: Linear;
CC Novel G protein-coupling receptor
FH Key Location/Qualifiers
FT source 1..969 /organism='Unidentified'.
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Best Local Similarity 98.8%; Pred. No. 1.2e-239;
Matches 957; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DB 61 ACTCCTGTCTACAGAGACCCCTGAGCTTCAAGGCTGACGTGCATCTTTCCCTTGTTC 120

QY 121 GCCTGACAGAAAGCGGTGTGCTCTGGCTCTGGCTGCGCATGCGCAGGAAACGCT 180
DB 121 GCCTGACAGAAAGCGGTGTGCTCTGGCTCTGGCTGCGCATGCGCAGGAAACGCT 180

QY 181 GTTCATCTACATCTCTCAACCTGTGCGGCGCATCTTCTCTTCTTACGGCCACATT 240
DB 181 GTTCATCTACATCTCTCAACCTGTGCGGCGCATCTTCTCTTCTTACGGCCACATT 240

QY 241 ATATGTTCCGCTTACCTCATCATATCCGCATCCCATCTCCAAATCTCTCAGTCT 300
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QY 301 GTGATGACCTTTCCCTATTATAGGCTTAAGCATGCTGAGGCCATGACACCGAGCGC 360
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DB 361 TGCTGTCCATCTGTGCGCCATCTGTTACCATGCTGCGCGCCGCCAGATCTGTCATCG 420

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QY 841 CGTCAAAATAGGAGACCTGAGCTGCTTCCAGAGGCTCTGAGGACACGCTGAG 900

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QY 901 GTGATGAGCTGAGGCTGCTTCTCAGGAAACCTGAGCTGTCGGAAACGATTTG 960

DB 901 GTGATGAGCTGAGGCTGCTTCTCAGGAAACCTGAGCTGTCGGAAACGATTTG 960

QY 961 GAGCAGTGA 969

DB 961 GAGCAGTGA 969

RESULT 15
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LOCUS Homo sapiens G protein-coupled receptor SNR2 gene, complete cds.
DEFINITION AF474988
ACCESSION AF474988
VERSION AF474988.2 GI:31747896
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS Lembo, P.M., Grazzini, E., Groblewski, T., O'Donnell, D., Roy, M.-O.,
Zhang, J., Hoffert, C., Cao, J., Schmidt, R., Pelletier, M., Labarre, M.,
Gosselin, M., Fortin, Y., Banville, D., Shen, S., Strom, P., Payza, K.,
Dray, A., Walker, P. and Ahmad, S.
TITLE Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs
JOURNAL Nat. Neurosci. 5 (3), 201-209 (2002)
MEDLINE 21853733
PUBMED 11850634
REFERENCE 2 (bases 1 to 969)
AUTHORS Ahmad, S., Banville, D., Fortin, Y., Lembo, P.M. and O'Donnell, D.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) Molecular Biology, AstraZeneca, 7171
Frederick-Banting, Montreal, Quebec H4S 1Z9, Canada
COMMENT On Jun 16, 2003 this sequence version replaced gi:19338909.
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 97.5%; Score 945; DB 9; Length 969;
Best Local Similarity 98.5%; Pred. No. 2.2e-238;
Matches 954; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 61 ACTCCTGTCTACAGAGACCCCTGAGCTTCAAGGCTGACGTGCATCTTTCCCTTGTTC 120


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QY      |||||
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QY      |||||
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961  GAGCAGTGA 969
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Job time : 4170 secs

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Run on: July 4, 2004, 04:47:27 ; Search time 478 Seconds
(without alignments)
8611.933 Million cell updates/sec

Title: US-09-787-879C-3
Perfect score: 969
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002s: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	969	100.0	969	3	AAA29811 Human G p
2	969	100.0	969	6	ABT04875 Human G p
3	969	100.0	1400	6	AAD33751 Human Mrq
4	969	100.0	1400	7	AB242595 Human G p
5	969	100.0	2618	6	ABX52822 CDNA enco
6	969	100.0	8622	6	ABX52823 Genomic D
7	967.4	99.8	969	3	AAA29812 Human G p
8	965.8	99.7	1369	3	ADC86820 Human GPC
9	964.2	99.5	969	3	AAD70342 Human nov
10	949.8	98.0	969	2	AAD10067 Human dor
11	938.6	96.9	969	2	AAD10068 Human dor
12	845.8	87.3	309	7	ACC44771 Human G p
13	837.8	86.5	969	9	AAD12208 Human G p
14	837.8	86.5	969	9	ADCL17729 Human TGR
15	836.2	86.3	969	2	AAZ10071 Human dor
16	834.6	86.1	969	3	AAZ12205 Human G p
17	834.6	86.1	969	9	ADCL17725 Human TGR
18	833	86.0	969	2	AAD10069 Human dor
19	833	86.0	969	3	AAZ12204 Human G p
20	833	86.0	969	6	ABT04874 Human G p
21	833	86.0	969	7	ACC44768 Human G p
22	833	86.0	969	9	ADCL17724 Human TGR
23	833	86.0	1369	9	ADC86588 Human GPC

24	833	86.0	1604	6	AAD33752 Human Mrq
25	833	86.0	1604	7	AB242602 Human Mrq
26	829.8	85.6	969	2	AAZ10072 Human G p
27	829.8	85.6	969	4	AAD20943 Human G p
28	829.8	85.6	969	5	AAZ07944 Human G p
29	829.8	85.6	969	6	AAD27494 Human G p
30	829.8	85.6	969	6	AB242891 Human GPC
31	829.8	85.6	969	7	ACC44772 Human G p
32	829.8	85.6	969	7	AB281334 Human Dor
33	829.8	85.6	969	9	AAD61647 Human GPC
34	829.8	85.6	1369	9	ADC86444 Human GPC
35	829.8	85.6	2040	6	AAD33744 Human Mrq
36	828.2	85.5	1116	4	AAH49507 Human GTP
37	826.6	85.3	969	2	AAZ10070 Human dor
38	798.8	82.4	912	9	ADCL12765 Human GPC
39	792.2	81.8	966	4	AAD20948 Human G p
40	780.2	80.5	973	4	AAK51462 Human pol
41	769.6	79.4	966	4	AAD20945 Human G p
42	729.4	75.3	1997	9	ADD18121 Human G-p
43	727.2	75.0	912	9	ADCL12761 Human GPC
44	697.4	72.0	769	6	AB235127 Human Gen
45	618.8	63.9	961	4	AAD20946 Human G p

ALIGNMENTS

RESULT 1

AAA29811
ID AAA29811 standard; cDNA; 969 BP.

XX
AC AAA29811;

XX
DT 18-AUG-2000 (first entry)

XX
DE Human G protein-coupled receptor hH17n213 encoding cDNA SEQ ID NO:3.

XX
KW Human; G protein-coupled receptor; hippocampus; diagnosis; screening; genetic disease; cellular function regulation; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT CDS 1..969

FT FT /*tag= a

XX
FT FT /product= "G protein-coupled receptor"

XX
PN WO200020455-A1.

XX
PD 13-APR-2000.

XX
PF 30-SEP-1999; 99WO-JP005366.

XX
PR 01-OCT-1998; 98JP-00279535.

XX
PA (TAKE) TAKEDA CHEM IND LTD.

XX
PI Watanabe T, Terao Y, Matsui H;

XX
DR WPI; 2000-303747/26.

XX
PT P-PSDB; AAY90761.

XX
PT Human-derived G protein-coupled protein and encoding nucleic acid, useful e.g. in determining ligands and treatment of diseases associated with dysfunction of the protein.

XX
PS Claim 6; Page 93-94; 97pp; Japanese.

XX
CC The present sequence encodes a human-derived G protein-coupled protein designated hH17n213, which is isolated from the human hippocampus. The G protein-coupled receptor can be used for preventing, treating and diagnosing genetic diseases associated with G protein-coupled protein, and for regulating cellular functions. The protein can be used to prevent

CC and treat disorders associated with G protein-coupled protein gene
CC dysfunction. It can also be used to identify G protein-coupled protein
CC ligands and generating antibodies and antisera against the protein. It is
CC also useful in constructing recombinant receptor protein expression
CC systems, developing receptor-binding assay systems and screening drug
CC candidates, and can be used as a probe in the genetic diagnosis of G
CC protein-coupled protein disorders
XX
SQ Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 969; DB 3; Length 969;
Best Local Similarity 100.0%; Pred. No. 7.3e-263;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGCTCTGGGTACAGAACTGACACCAATCAACGGAGTGGAGG 60
DB 1 ATGGATTCAACCATCCAGCTCTGGGTACAGAACTGACACCAATCAACGGAGTGGAGG 60
QY 61 ACTCCTTGCTACAGAGACCCCTGAGCTTCACGGGCTGACGTGATCGTTTCCCTTGTG 120
DB 61 ACTCCTTGCTACAGAGACCCCTGAGCTTCACGGGCTGACGTGATCGTTTCCCTTGTG 120
QY 121 GCGCTGACAGAAACGGGTGTGCTCTGGCTCTGGCTGCGGCTGCGGATGCGAGGACGCT 180
DB 121 GCGCTGACAGAAACGGGTGTGCTCTGGCTCTGGCTGCGGCTGCGGATGCGAGGACGCT 180
QY 181 GTCTCCATCTACATCTCAACCTGCTCGGCGGCTGCTCTCTCTTCTTACGCGCCACATT 240
DB 181 GTCTCCATCTACATCTCAACCTGCTCGGCGGCTGCTCTCTCTTCTTACGCGCCACATT 240
QY 241 ATATGTCGCGGTAGCCCTCATCAATATCCGCTCCCTCATCTCCAAATCTCTGCTCT 300
DB 241 ATATGTCGCGGTAGCCCTCATCAATATCCGCTCCCTCATCTCCAAATCTCTGCTCT 300
QY 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGACCGAGCG 360
DB 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGACCGAGCG 360
QY 361 TGCGTGTCCATCTGTGCGCCATCTGTACATCTGCGGCTGCGGCTGCGGATGCGATGTC 420
DB 361 TGCGTGTCCATCTGTGCGCCATCTGTACATCTGCGGCTGCGGCTGCGGATGCGATGTC 420
QY 421 GTCATGTGTCTGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCTG 480
DB 421 GTCATGTGTCTGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCTG 480
QY 481 TGTGACTTCTGTTAGTGTGCTGATCTGTTGTGTAACCGTCAATTTTCAATACA 540
DB 481 TGTGACTTCTGTTAGTGTGCTGATCTGTTGTGTAACCGTCAATTTTCAATACA 540
QY 541 ATCGCTGCTGCTGTTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 ATCGCTGCTGCTGTTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 AGGATCTCTGTGATCCGGAAGATCGCGTGTACAGAGCTGTACGTGACCATCTCTCTC 660
DB 601 AGGATCTCTGTGATCCGGAAGATCGCGTGTACAGAGCTGTACGTGACCATCTCTCTC 660
QY 661 ACAGTGTGCTGCT 720
DB 661 ACAGTGTGCTGCT 720
QY 721 AGGATCCACCTGGATGAAAGTCTTATTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 AGGATCCACCTGGATGAAAGTCTTATTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TCCGCTCTTACAGAGTGCACCCCATCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
DB 781 TCCGCTCTTACAGAGTGCACCCCATCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 841 CGTCAAAATAGGAGAACTGAAGCTGTTTCTCCAGAGGCTCTGACGAGCACGCTGAG 900
DB 841 CGTCAAAATAGGAGAACTGAAGCTGTTTCTCCAGAGGCTCTGACGAGCACGCTGAG 900

QY 901 GTGGATCAAGTGGAGGCTGCTCTCTCAGGAAACCTCGAGCTGTGCGGAACGAGATTG 960
DB 901 GTGGATCAAGTGGAGGCTGCTCTCTCAGGAAACCTCGAGCTGTGCGGAACGAGATTG 960
QY 961 GAGCAGTGA 969
DB 961 GAGCAGTGA 969

RESULT 2
ABT04875

ID ABT04875 standard; cDNA; 969 BP.

XX ABT04875;

AC AC (first entry)

DT 11-OCT-2002 (first entry)

XX Human G protein coupled receptor hRUP37 coding sequence.

DE Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;

KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.

XX Homo sapiens.

OS WO200242451-A2.

PN 30-MAY-2002.

XX 26-NOV-2001; 2001WO-US044386.

XX 27-NOV-2000; 2000US-0253404P.

PR 12-DEC-2000; 2000US-0253366P.

PR 20-FEB-2001; 2001US-0270286P.

PR 06-APR-2001; 2001US-0282032P.

PR 06-APR-2001; 2001US-0282358P.

PR 06-APR-2001; 2001US-0282365P.

PR 14-MAY-2001; 2001US-0290917P.

PR 31-JUL-2001; 2001US-0309208P.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;

XX WPI: 2002-566565/50.

XX P-PSDB; ABC04077.

XX Novel endogenous and non-endogenous versions of G protein-coupled

PT receptor useful for identification of candidate compounds as receptor

PT agonists or antagonists for use as therapeutic agents.

XX Claim 39; Page 74; 84pp; English.

XX The present invention provides the protein and coding sequences of

CC several human G-protein coupled receptors (GPCRs). These can be used in

CC the identification of candidate compounds as receptor agonists or inverse

CC agonists having applicability as therapeutic agents. The present sequence

CC is a GPCR coding sequence of the invention

XX Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 969; DB 6; Length 969;

Best Local Similarity 100.0%; Pred. No. 7.3e-263;

Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGCTCTGGGTACAGAACTGACACCAATCAACGGAGTGGAGG 60

DB 1 ATGGATTCAACCATCCAGCTCTGGGTACAGAACTGACACCAATCAACGGAGTGGAGG 60

QY 61 ATCCCTTGCTACAGAGACCCCTGAGCTTACGGGCTGAGTGCATGTTTCCCTTCTC 120


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QY 361 TGCCTGTCATCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 420
Db 692 TGCCTGTCATCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 751
QY 421 GTCATGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 480
Db 752 GTCATGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 811
QY 481 TGTGACTTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 540
Db 812 TGTGACTTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 871
QY 541 ATCGGTGTCGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 600
Db 872 ATCGGTGTCGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 931
QY 601 AGGATTCCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 660
Db 932 AGGATTCCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 991
QY 661 ACAGTGTCTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 720
Db 992 ACAGTGTCTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 1051
QY 721 AGGATTCCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 780
Db 1052 AGGATTCCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 1111
QY 781 TCCGCTCTTTACAGCAGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 840
Db 1112 TCCGCTCTTTACAGCAGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 1171
QY 841 CCTCAAAATAGCAGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 900
Db 1172 CCTCAAAATAGCAGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 1231
QY 901 GTGGATGAAGTGTGGAGGTGGCTTCTCTCAGGAAACCTCTGAGCTGTCTGAGGAGCAGATTTG 960
Db 1232 GTGGATGAAGTGTGGAGGTGGCTTCTCTCAGGAAACCTCTGAGCTGTCTGAGGAGCAGATTTG 1291
QY 961 GAGCAGTGA 969
Db 1292 GAGCAGTGA 1300

RESULT 5
ID ABK52822 standard; cDNA; 2618 BP.
AC ABK52822;
XX
DT 27-AUG-2002 (first entry)
XX
DE cDNA encoding human G-protein coupled receptor (GPCR).
XX
KW Human; G-protein coupled; receptor; GPCR; human protease;
KW human therapeutic protein; query sequence; search; gene; ss;
KW sequence database; non-human transgenic animal; gene therapy;
XX chromosome 3.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 447..1460
FT /*tag= a
FT /product= "Human G-protein coupled receptor (GPCR)"
XX
PN W0200234914-A1.
XX
XX 02-MAY-2002.
XX
XX 10-OCT-2001; 2001WO-US031592.
XX
PF
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XX
PR 25-OCT-2000; 2000US-00695045.
PR 31-MAY-2001; 2001US-00867570.
XX
PA (PEKE ) PE CORP NY.
XX
XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;
PI P-PSDB; AAU97598.
XX
XX WPI; 2002-463360/49.
XX
DR P-PSDB; AAU97598.
XX
XX Novel isolated G-protein coupled receptor peptide useful for treating
PT disorder characterized by absence of, in appropriate or unwanted
PT expression of the receptor protein, and as immunogens to raise
PT antibodies.
XX
XX Claim 4; Fig 1; 75pp; English.
XX
XX The present invention relates to a new G-protein coupled receptor (GPCR)
CC peptide. The invention is useful for identifying a modulator of GPCR and
CC for treating a disease or condition mediated by a human protease. The
CC invention is also useful as models for the development of human
CC therapeutics, for identifying therapeutic proteins, as targets for
CC development of human therapeutic agents, and as query sequence to perform
CC a search against sequence databases to, for e.g., identify other family
CC members of related sequences. The vector of the invention is useful for
CC producing a GPCR protein or peptide, for conducting cell-based assays
CC involving the GPCR protein or its fragment, for identifying GPCR protein
CC mutants whose functions are affected, and to produce non-human transgenic
CC animals. The present nucleic acid sequence represents the human G-protein
CC coupled receptor (GPCR) gene located on chromosome 3. This sequence
CC encodes the human G-protein coupled receptor (GPCR) protein of the
CC invention
XX
SQ Sequence 2618 BP; 655 A; 637 C; 546 G; 780 T; 0 U; 0 Other;
Query Match 100.0%; Score 969; DB 6; Length 2618;
Best Local Similarity 100.0%; Pred. No. 1.2e-262;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 492 ATGGATTCAACCATCCACGCTTTGGGTACAGACTGACACCAATCAACGACCTGAGGAG 551
QY 61 ACTCTTTGTACAGACGACCTGAGCTTCAAGGCTGACGCTGATCGTTTCCCTTGTTC 120
Db 552 ACTCTTTGTACAGACGACCTGAGCTTCAAGGCTGACGCTGATCGTTTCCCTTGTTC 611
QY 121 GCGCTGACAGAAACGCGGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 612 GCGCTGACAGAAACGCGGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
QY 181 GTCTCCATCTACATCTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 672 GTCTCCATCTACATCTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
QY 241 ATATGTTGCGGTTTACGCTTCATCAATATCGGCTATCCCATCTCCAAATCCCTCAGTCT 300
Db 732 ATATGTTGCGGTTTACGCTTCATCAATATCGGCTATCCCATCTCCAAATCCCTCAGTCT 791
QY 301 GTGATGACCTTTTCCCTTACTTTATAGGCTTAAGCATGCTGAGCGCCATCAACGACGCGC 360
Db 792 GTGATGACCTTTTCCCTTACTTTATAGGCTTAAGCATGCTGAGCGCCATCAACGACGCGC 851
QY 361 TGCCTGTCTCATCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 420
Db 852 TGCCTGTCTCATCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 911
QY 421 GTCATGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 480
Db 912 GTCATGTGTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 971
QY 481 TGTGACTTCTCTCTGCGCCCATCTGTTACCACTGCCCGCCGCCAGATACCTGTCTATCG 540
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Db 972 TGTGACTTCTCTGTTAGTGGTCTGATCTGTTGGTGTGAACGTGAGATTTCAATACA 1031
QY 541 ATCGAGTGGCTGGTGTGTTTATGCTGCTTCTGTGGTCCAGCCTGCTCTGCTGGTC 600
Db 1032 ATCGAGTGGCTGGTGTGTTTATGCTGCTTCTGTGGTCCAGCCTGCTCTGCTGGTC 1091
QY 601 AGGATTTCTGTGGATCCCGAAGATGCCGTGACCGAGGTGTGACGTGACCATCTCTCCTC 660
Db 1092 AGGATTTCTGTGGATCCCGAAGATGCCGTGACCGAGGTGTGACGTGACCATCTCTCCTC 1151
QY 661 ACAGTGGCTGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 1152 ACAGTGGCTGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
QY 721 AGGATCCACTGGATGGAAGTCTTATTTGTGATGTGATCTGATTTCCATTTTCTCTG 780
Db 1212 AGGATCCACTGGATGGAAGTCTTATTTGTGATGTGATCTGATTTCCATTTTCTCTG 1271
QY 781 TCCGCTCTTAACAGCAGTGGCAACCCCATCAATTTACTTCTTCGTGGGCTCTTTAGGCAG 840
Db 1272 TCCGCTCTTAACAGCAGTGGCAACCCCATCAATTTACTTCTTCGTGGGCTCTTTAGGCAG 1331
QY 841 COTCAAAATAGCAGAACCTGAAGTGTCTTCCAGAGGCTCTGACAGGACACGCTCTGAG 900
Db 1332 COTCAAAATAGCAGAACCTGAAGTGTCTTCCAGAGGCTCTGACAGGACACGCTCTGAG 1391
QY 901 GTGGATGAAGTGGAGGTGGCTTCTCAGGAACCTGGAGTGTGCGGAACGACATG 960
Db 1392 GTGGATGAAGTGGAGGTGGCTTCTCAGGAACCTGGAGTGTGCGGAACGACATG 1451
QY 961 GAGCAGTGA 969
Db 1452 GAGCAGTGA 1460

RESULT 6

ABK52823
ID ABK52823 standard; DNA; 8622 BP.

AC ABK52823;
XX

DT 27-AUG-2002 (first entry)

XX Genomic DNA encoding human G-protein coupled receptor (GPCR).

DE Human: G-protein coupled; receptor; GPCR; human protease;
XX human therapeutic protein; query sequence; search; gene; ds;
KW sequence database; non-human transgenic animal; gene therapy;
KW chromosome 3.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 4300..8496
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FT /*tag= a
FT /product= "Human G-protein coupled receptor (GPCR)"
FT 4300..4319

FT /*tag= b
FT /number= 1

FT /*tag= c
FT /number= 1

FT /*tag= d
FT /number= 2

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PR

PR 25-OCT-2000; 2000US-00695045.

XX 31-MAY-2001; 2001US-00867570.

XX (PEKE) PE CORP NY.

XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;

XX WPI; 2002-463360/49.

XX P-PSDB; AAU97598.

XX Novel isolated G-protein coupled receptor peptide useful for treating

XX disorder characterized by absence of, in appropriate or unwanted

XX expression of the receptor protein, and as immunogens to raise

XX antibodies.

XX Claim 4; Fig 3; 75pp; English.

XX The present invention relates to a new G-protein coupled receptor (GPCR)

XX peptide. The invention is useful for identifying a modulator of GPCR and

XX for treating a disease or condition mediated by a human protease. The

XX invention is also useful as models for the development of human

XX therapeutics, for identifying therapeutic proteins, as targets for

XX a search against sequence databases to, for e.g., identify other family

XX members of related sequences. The vector of the invention is useful for

XX producing a GPCR protein or peptide, for conducting cell-based assays

XX involving a GPCR protein or its fragment, for identifying GPCR protein

XX mutants whose functions are affected, and to produce non-human transgenic

XX animals. The present nucleic acid sequence represents the human G-protein

XX coupled receptor (GPCR) gene located on chromosome 3. This sequence

XX encodes the human G-protein coupled receptor (GPCR) protein of the

XX invention

XX SQ Sequence 8622 BP; 2684 A; 1921 C; 1679 G; 2338 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 969; DB 6; Length 8622;

XX Best Local Similarity 100.0%; Pred. No. 28-262;

XX Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGTGGAG 60

Db 7528 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGTGGAG 7587

QY 61 ACTCTTGTCTACAGCAGACCTTACGCGGCTGACGCTGATCGTTTCCCTTTC 120

Db 7588 ACTCTTGTCTACAGCAGACCTTACGCGGCTGACGCTGATCGTTTCCCTTTC 7647

QY 121 GCGTGTACAGAAACCGGTTGTCTCTGCTCTGGGCTGCGGATGCGCAGGAACT 180

Db 7648 GCGTGTACAGAAACCGGTTGTCTCTGCTCTGGGCTGCGGATGCGCAGGAACT 7707

QY 181 GTCTCCATCTACATCTCAACCTGTCGCGGCTGCTCTCTTCTAGCGGCGACATT 240

Db 7708 GTCTCCATCTACATCTCAACCTGTCGCGGCTGCTCTCTTCTAGCGGCGACATT 7767

QY 241 ATATGTTGCGGTTAGCCTCAATATCCGCAATCCCATCTCCAAATCTCTAGTCT 300

Db 7768 ATATGTTGCGGTTAGCCTCAATATCCGCAATCCCATCTCCAAATCTCTAGTCT 7827

QY 301 GTGATGACCTTTCCCTACTTTATAGCCCTAAGCATGCTGAGCCCATGACGACCGAG 360

Db 7828 GTGATGACCTTTCCCTACTTTATAGCCCTAAGCATGCTGAGCCCATGACGACCGAG 7887

QY 361 TGCTGTCCATCTCTGTGGGCTGCTGTGATACCTGCGCGGCGCCGAGATCTGTCTAT 420

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QY 421 GTCATGTGTCTCTGTGGGCTGCTGTGATACCTGCGCGGCTGCTGTGATGCTGTC 480

Db 7948 GTCATGTGTCTCTGTGGGCTGCTGTGATACCTGCGCGGCTGCTGTGATGCTGTC 8007

QY 481 TGTGACTTCTGTTTGTGCTGCTGATCTCTGTTTGTGTAACGTCAGATTTCAATACA 540

QY 781 TCCGCTCTTAACACAGTGCACACCCCATCAATTACTTCTTCTGCGGCTCCCTTTAGGCAG 840
 Db 781 TCCGCTCTTAACACAGTGCACACCCCATCAATTACTTCTTCTGCGGCTCCCTTTAGGCAG 840
 QY 841 CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGACGACACGCTGAG 900
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 QY 961 GAGCAGTGA 969
 Db 961 GAGCAGTGA 969

RESULT 8

ADC86820
 ID ADC86820 standard; DNA; 1369 BP.

XX AC ADC86820;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR gene SEQ ID NO:1273.

XX KW ds; gene; human; GPCR;

XX KW Guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX OS Homo sapiens.

XX PN BP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX DR WPI; 2003-315783/31.

XX DR P-PSDB; ADC86821.

XX PT New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.

XX PS Claim 1; SEQ ID NO 1273; 28pp; English.

XX CC The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the invention.

XX SQ Sequence 1369 BP; 272 A; 372 C; 340 G; 385 T; 0 U; 0 Other;

Query Match

Best Local Similarity 99.7%; Score 965.8; DB 9; Length 1369;

Matches 967; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
 Db 201 ATGGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 260

QY 61 ACTCCTTCTCTAAACAGACCCCTGAGTTTCAOGGGGTGACGTGCATCGTTTCCCTTGTTC 120
 Db 261 ACTCCTTCTCTAAACAGACCCCTGAGTTTCAOGGGGTGACGTGCATCGTTTCCCTTGTTC 320
 QY 121 GGGCTGACAGAAACCGGTTTGTCTCTGGCTCTCTGGGCTGCCGATGCCGACGAAACGCT 180
 Db 321 GGGCTGACAGAAACCGGTTTGTCTCTGGCTCTCTGGGCTGCCGATGCCGACGAAACGCT 380
 QY 181 GTCTCATCTACATCTCACTGCTGGTGGCGGCGACHTTCTCTTCTTTAGCGGCACATT 240
 Db 381 GTCTCATCTACATCTCACTGCTGGTGGCGGCGACHTTCTCTTCTTTAGCGGCACATT 440
 QY 241 ATATGTTCCCGGTTACGGCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT 300
 Db 441 ATATGTTCCCGGTTACGGCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT 500
 QY 301 GTGATGACCTTTCCTACTTTATAGGCTAAGCATGTGAGCGCATGAGCGGACGAGCGC 360
 Db 501 GTGATGACCTTTCCTACTTTATAGGCTAAGCATGTGAGCGCATGAGCGGACGAGCGC 560
 QY 361 TGCCTGTCCATCTGTGTGCCCATCTGTGACACATGCCCGCGCCGCCAGATACCTGTATCG 420
 Db 561 TGCCTGTCCATCTGTGTGCCCATCTGTGACACATGCCCGCGCCGCCAGATACCTGTATCG 620
 QY 421 GTCATGTGTCTCTGCTCTGGGCGCTGTCCCTGTGGGAGTATCCTTGGAGTGGATGTTTC 480
 Db 621 GTCATGTGTCTCTGCTCTGGGCGCTGTCCCTGTGGGAGTATCCTTGGAGTGGATGTTTC 680
 QY 481 TGTGACTTCCCTGTTTAGTGTGCTGATTCTGTGTTGGTGAAACGTCAGATTTCAATACA 540
 Db 681 TGTGACTTCCCTGTTTAGTGTGCTGATTCTGTGTTGGTGAAACGTCAGATTTCAATACA 740
 QY 541 ATCGGGTGGCTGTTTATGTTGTTCTCTGTGGGTCCAGCCCTGGTCTGCTGCTGCTC 600
 Db 741 ATCGGGTGGCTGTTTATGTTGTTCTCTGTGGGTCCAGCCCTGGTCTGCTGCTGCTC 800
 QY 601 AGGATTCTGTGATGCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTTCTCTC 660
 Db 801 AGGATTCTGTGATGCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTTCTCTC 860
 QY 661 ACAGTGTCTGCTTCT 720
 Db 861 ACAGTGTCTGCTTCT 920
 QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTGTGATGTCATGTGATCTAGTTCCATTTCC 780
 Db 921 AGGATCCACCTGGATTGGAAGTCTTATTTGTGATGTCATGTGATCTAGTTCCATTTCC 980
 QY 781 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 840
 Db 981 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 1040
 QY 841 CGTCAAAATAGGCAGAACCTGAGCTGGTCTCCAGAGGGCTCTGCAGGACACGCTGAG 900
 Db 1041 CGTCAAAATAGGCAGAACCTGAGCTGGTCTCCAGAGGGCTCTGCAGGACACGCTGAG 1100
 QY 901 GTGGATGAAGTGGAGGTGGCTTCTCAGAAACCTCGAGCTGTGCGGAGACAGATTG 960
 Db 1101 GTGGATGAAGTGGAGGTGGCTTCTCAGAAACCTCGAGCTGTGCGGAGACAGATTG 1160
 QY 961 GAGCAGTGA 969
 Db 1161 GAGCAGTGA 1169

RESULT 9

AAA70342

ID AAA70342 standard; cDNA; 969 BP.

XX AC AAA70342;

XX DT 19-DEC-2000 (first entry)

XX DE Human novel G-protein coupled receptor #1 coding sequence.
 XX DE Human; novel G-protein coupled receptor; signal transduction;
 XX KW disease diagnosis; drug screening; disease therapy; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..969
 XX FT /*tag= a
 XX FT /product= "novel G-protein coupled receptor #1"
 XX PN WO200040724-A1.
 XX PD 13-JUL-2000.
 XX PF 04-JAN-2000; 2000WO-US000052.
 XX PR 04-JAN-1999; 99US-0114666P.
 XX PR 14-JAN-1999; 99US-0115828P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX PA Nehls M, Wattler F;
 XX PI WPI: 2000-465986/40.
 XX DR P-PSDB; AAB14846.
 XX PT New polynucleotides encoding novel G-protein coupled receptors useful for
 XX PT diagnosis, drug screening, clinical trial monitoring and for the
 XX PT treatment of physiological or behavioral disorders.
 XX PS Claim 1; Page 52-53; 61pp; English.
 XX CC The present sequence is the coding sequence for a novel human G-protein
 XX CC coupled receptor (NGPCR). These proteins are involved in signal
 XX CC transduction pathways in many cases. The protein contains seven
 XX CC transmembrane domains, and is expressed in human testis, mammary gland
 XX CC and salivary gland tissue. The gene, its protein, agonists, antagonists
 XX CC and antibodies can be used to diagnose and treat diseases associated with
 XX CC the inappropriate expression or expression of mutant versions of the
 XX CC protein, for screening for drugs which can be used in the same manner,
 XX CC and for elucidating the function of the protein
 XX SQ Sequence 969 BP; 172 A; 282 C; 249 G; 266 T; 0 U; 0 Other;

Query Match 99.5%; Score 964.2; DB 3; Length 969;
 Best Local Similarity 99.7%; Pred. No. 1.7e-261;
 Matches 966; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGATTCACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
 DB 1 ATGGATTCACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
 QY 51 ACTCTTCTACAGCAGACCCCTGAGCTTACGGGGCTGAGTGCATGCTTCCCTGTC 120
 DB 51 ACTCTTCTACAGCAGACCCCTGAGCTTACGGGGCTGAGTGCATGCTTCCCTGTC 120
 QY 121 GCGTGTACAGGAACCGCGTGTGTCTGTGGTCTCTGGGCTCCCGCATGCGCAGGAACGCT 180
 DB 121 GCGTGTACAGGAACCGCGTGTGTCTGTGGTCTCTGGGCTCCCGCATGCGCAGGAACGCT 180
 QY 181 GTCTCCATCTACATCTCAACTGTGTGCGGCGGACATCTCTTCTTAGGGCCACATT 240
 DB 181 GTCTCCATCTACATCTCAACTGTGTGCGGCGGACATCTCTTCTTAGGGCCACATT 240
 QY 241 ATATGTTCCGGTTCACGCTTCATCAATACCGCATCCCATCTCCAAAATCCTCAGTCCT 300
 DB 241 ATATGTTCCGGTTCACGCTTCATCAATACCGCATCCCATCTCCAAAATCCTCAGTCCT 300
 QY 301 GTGATGACCTTTCCTACTTATAGGCGCTAAGCATGCTGAGCGGCATCAGCCGAGGC 360

DB 301 GTGATGACCTTTCCTACTTTATAGGCGCTAAGCATGCTGAGCGGCATCAGCACCGAGGC 360
 QY 361 TGCCTGTCCATCTCTGTGGCCCATCTGTGTACCACTGCGCGCCGCCCCAGATACCTGTGTCG 420
 DB 361 TGCCTGTCCATCTCTGTGGCCCATCTGTGTACCACTGCGCGCCGCCCCAGATACCTGTGTCG 420
 QY 421 GTCATGTGTGTCCTGCTCTGGGCGCTGTCCCTGTGGGAGTATCCCTGGAGTGGATGTC 480
 DB 421 GTCATGTGTGTCCTGCTCTGGGCGCTGTCCCTGTGGGAGTATCCCTGGAGTGGATGTC 480
 QY 481 TGTGACTTCTCTGTTTAGTGGTGTCTCTGTTGGTGTGAAAGCTCAGATTTTCATTACA 540
 DB 481 TGTGACTTCTCTGTTTAGTGGTGTCTCTGTTGGTGTGAAAGCTCAGATTTTCATTACA 540
 QY 541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTCTCTGTGGGTCAGGCTGCTCTGCTGTC 600
 DB 541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTCTCTGTGGGTCAGGCTGCTCTGCTGTC 600
 QY 601 AGGATTCTCTGTGGATCCCGGAAGATGCGGTGACCCAGGCTGTACGTGACCATCTCTCCTC 660
 DB 601 AGGATTCTCTGTGGATCCCGGAAGATGCGGTGACCCAGGCTGTACGTGACCATCTCTCCTC 660
 QY 661 ACAGTGTGGTCTCTCTCTGTGGCTGCGCTTGTGCATTCACTGGGCGCTGTTTTTC 720
 DB 661 ACAGTGTGGTCTCTCTCTGTGGCTGCGCTTGTGCATTCACTGGGCGCTGTTTTTC 720
 QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTGTATGTGCACTAGTTTCCATTTTCCTG 780
 DB 721 AGGATCCACCTGGATTGGAAGTCTTATTTGTATGTGCACTAGTTTCCATTTTCCTG 780
 QY 781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCATTTACTTCTCGTGGGCTCTCTTAGGAG 840
 DB 781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCATTTACTTCTCGTGGGCTCTCTTAGGAG 840
 QY 841 CCTCAAAATAGCAGAACCTGAAGCTGTTCTCCAGAGGGCTCTGACGACACGCTGAG 900
 DB 841 CCTCAAAATAGCAGAACCTGAAGCTGTTCTCCAGAGGGCTCTGACGACACGCTGAG 900
 QY 901 GTGATGATGAGTGGAGGTGGCTTCTCCTCAGGAACCCCTGGAGCTGTCCGGGAAGCAGATTG 960
 DB 901 GTGATGATGAGTGGAGGTGGAGGCTTCTCCTCAGGAACCCCTGGAGCTGTCCGGGAAGCAGATTG 960
 QY 961 GAGCAGTGA 969
 DB 961 GAGCAGTGA 969

RESULT 10
 AAZ10067
 ID AAZ10067 standard; DNA; 969 BP.
 XX AAZ10067;
 AC AC
 XX 20-MAR-2003 (revised)
 DT 26-NOV-1999 (first entry)
 XX Human dorsal root receptor 1 hDRR1 nucleotide sequence.
 DE Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
 KW hDRR1; central nervous system; CNS; anaesthesia; analgesia; neuron;
 KW pain. ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..969
 XX FT /*tag= a
 XX FT /product= "hDRR1"
 XX FT /note= "Human dorsal root receptor 1"
 XX PN WO9932519-A1.
 XX PD 01-JUL-1999.

XX 16-DEC-1998; 98WO-SE002348.
 XX 22-DEC-1997; 97SE-00004836.
 XX (ASTR) ASTRA PHARMA INC.
 XX (ASTR) ASTRA AB.
 XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
 XX WPI; 1999-405162/34.
 XX P-PSDB; AAY30159.
 XX Rat and human dorsal root receptors and related polynucleotides, useful
 XX for identifying agents for anesthesia and analgesia.
 XX Claim 10; Page 42-43; 72pp; English.
 XX This is the human dorsal root receptor 1 (hDRR1) nucleotide sequence.
 XX hDRR1 is a G protein coupled receptor that is expressed preferentially in
 XX dorsal root ganglia. hDRR1 can be used to create antibodies against
 XX hDRR1. The dorsal root ganglia area of the central nervous system (CNS)
 XX is densely innervated with primary or afferent neurons involved in
 XX transmission, modulation and sensation of pain. The DR's which are
 XX expressed in this region of the CNS may be used for assays for the
 XX identification of new agents for anaesthesia and analgesia. (Updated on
 XX 20-MAR-2003 to correct PA field.)
 XX Sequence 969 BP; 179 A; 283 C; 239 G; 268 T; 0 U; 0 Other;

Query Match 98.0%; Score 949.8; DB 2; Length 969;
 Best Local Similarity 98.8%; Pred. NO. 1.9e-257;
 Matches 957; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGATTACACCTCCAGCTTTGGGTACAGAACTGACACCAATCAAGGACGTGAGAG 60
 DB 1 ATGGATCCACCTCCAGCTTTGGGTACAAACTGACACCAATCAAGGACGTGAGAG 60
 QY 61 ACTCTTGTACAAAGACAGACCTTGACCTTCAAGGGCTGACGTGATCTTCCCTGTC 120
 DB 61 ACTCTTGTACAAAGACAGACCTTGACCTTCAAGGGCTGACGTGATCTTCCCTGTC 120
 QY 121 GCGGTGACAGAAACGGGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 121 GCGGTGACAGAAACGGGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 181 GTCTCCATCTACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 GTCTCCATCTACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 ATATGTTGCGCGTTAGCGCTTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCT 300
 DB 241 ATATTTTCGCGTTAGCGCTTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCT 300
 QY 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCATCAGACCGAGCGC 360
 DB 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCATCAGACCGAGCGC 360
 QY 361 TGCCTGTCCATCTCTGTGCGCCATCTGTATACCACTGCGCGCGCCCGCCAGATACCTGTATCG 420
 DB 361 TGCCTGTCCATCTCTGTGCGCCATCTGTATACCACTGCGCGCGCCCGCCAGATACCTGTATCG 420
 QY 421 GTCATGTGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 421 GTCATGTGCTGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 481 TGTGACTTCCCTGTTAGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
 DB 481 TGTGACTTCCCTGTTAGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
 QY 541 ATCCGCTGGCTGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 541 ATCCGCTGGCTGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 601 AGGATTCCTCTGTGATCCCGAAGATGCGCTGACAGGCTGACGTGACCATCTCTCTC 660
 DB 601 AGGATTCCTCTGTGATCCCGAAGATGCGCTGACAGGCTGACGTGACCATCTCTCTC 660
 QY 661 ACAGTGTGCT 720
 DB 661 ACAGTGTGCT 720
 QY 721 AGGATCCACCTGATTCGAAAGTCTTATTTGTTCATGTGATCTAGTTCATTTTCTG 780
 DB 721 AGGATCCACCTGATTCGAAAGTCTTATTTGTTCATGTGATCTAGTTCATTTTCTG 780
 QY 781 TCCGCTCTTAACACAGATGCAACCCCATCATTTACTTCTCTGCTGCTCTCTCTCTG 840
 DB 781 TCCGCTCTTAACACAGATGCAACCCCATCATTTACTTCTCTGCTGCTCTCTCTCTG 840
 QY 841 CGTCAAAATAGCGAAGACCTGAAAGCTGTTCTCTCAGAGGCTCTGCGAGACACGCTGAG 900
 DB 841 CGTCAAAATAGCGAAGACCTGAAAGCTGTTCTCTCAGAGGCTCTGCGAGACACGCTGAG 900
 QY 901 GTGATGAGGTGAGGCTGCTCTCTCAGAAACCTGAGCTGCTGCGGAGCAGATG 960
 DB 901 GTGATGAGGTGAGGCTGCTCTCTCAGAAACCTGAGCTGCTGCGGAGCAGATG 960
 QY 961 GAGCAGTCA 969
 DB 961 GAGCAGTCA 969

RESULT 11

AAZ10068
 ID AAZ10068 standard; DNA; 969 BP.

XX AAZ10068;

XX AC
 XX 20-MAR-2003 (revised)
 XX 26-NOV-1999 (first entry)

XX Human dorsal root receptor 2 hDRR2 nucleotide sequence.

XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
 XX hDRR2; central nervous system; CNS; anaesthesia; analgesia; neuron;
 XX pain. ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..969

XX FT /*tag= a
 XX FT /product= "hDRR2"
 XX FT /note= "Human dorsal root receptor 2"

XX WO9932519-A1.

XX 01-JUL-1999.

XX 16-DEC-1998; 98WO-SE002348.

XX 22-DEC-1997; 97SE-00004836.

XX (ASTR) ASTRA PHARMA INC.

XX (ASTR) ASTRA AB.

XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;

XX WPI; 1999-405162/34.

XX P-PSDB; AAY30160.

XX Rat and human dorsal root receptors and related polynucleotides, useful
 XX for identifying agents for anesthesia and analgesia.

XX Claim 15; Page 46-47; 72pp; English.

XX	SQ	Sequence	909 BP;	163 A;	260 C;	234 G;	252 T;	0 U;	0 Other;
Query Match		87.3%;	Score	845.8;	DB	7;	Length	909;	
Best Local Similarity		99.8%;	Pred. No.	4.2e-228;					
Matches	847;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	121	GGCGTCAGAGAAACGGGTTGTCTCTGGCTCTGGCTGCGCATGCGCAGGAACGCT	180						
DB	61	GGCGTCAGAGAAACGGGTTGTCTCTGGCTCTGGCTGCGCATGCGCAGGAACGCT	120						
QY	181	GTCTCCATCTACATCCTCAACCTGGTCGCGCGCGCATTCCTCTTCCTTAGCGGCGCACATT	240						
DB	121	GTCTCCATCTACATCCTCAACCTGGTCGCGCGCGCATTCCTCTTCCTTAGCGGCGCACATT	180						
QY	241	ATATGTTGCGGTTACGCTCATCAATATCGGCATCCCATCTCCAAATATCTCAGTCCT	300						
DB	181	ATATGTTGCGGTTACGCTCATCAATATCGGCATCCCATCTCCAAATATCTCAGTCCT	240						
QY	301	GTGATGACCTTTCCCTACTTTATAGGCTAAGCATGCTAGCGCCATCAGACCCAGGCGC	360						
DB	241	GTGATGACCTTTCCCTACTTTATAGGCTAAGCATGCTAGCGCCATCAGACCCAGGCGC	300						
QY	361	TGCGTGTGCATCCTGTGCGCCATCTGGTACACATGCGCGCGCGCCACAGATCTGTCATCG	420						
DB	301	TGCGTGTGCATCCTGTGCGCCATCTGGTACACATGCGCGCGCGCCACAGATCTGTCATCA	360						
QY	421	GTCACTGTGTCTCTGCTCTGCGGCCCTGTGCCCTGTGCGAGTATCTGAGTGGATGTC	480						
DB	361	GTCACTGTGTCTCTGCTCTGCGGCCCTGTGCCCTGTGCGAGTATCTGAGTGGATGTC	420						
QY	481	TGTGACTTCTCTTTAGTGGTCTGAATCTGTTTGGTGTGAAACGTCAGATTCATTACA	540						
DB	421	TGTGACTTCTCTTTAGTGGTCTGAATCTGTTTGGTGTGAAACGTCAGATTCATTACA	480						
QY	541	ATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGTCCAGCCTGGTCTGGTGC	600						
DB	481	ATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGTCCAGCCTGGTCTGGTGC	540						
QY	601	AGGATTCTCTGTGGATCCCGAAGATCGCGTGCACAGGCTGTACGTGACCATCTCTCTC	660						
DB	541	AGGATTCTCTGTGGATCCCGAAGATCGCGTGCACAGGCTGTACGTGACCATCTCTCTC	600						
QY	661	ACAGTCTGGCTTCTCTCTGTGGCTGCGCTTTGGCATTCAGTGGGCGCTGTTTCC	720						
DB	601	ACAGTCTGGCTTCTCTCTGTGGCTGCGCTTTGGCATTCAGTGGGCGCTGTTTTC	660						
QY	721	AGGATCCACTGATTGGAAAGTCTTATTTGTGTCATGTGCATCTAGTTTCCATTTTCCTG	780						
DB	661	AGGATCCACTGATTGGAAAGTCTTATTTGTGTCATGTGCATCTAGTTTCCATTTTCCTG	720						
QY	781	TCCGCTCTTAAACAGCAGTGCACACCCCATCAATTACTTCTGTGGGCTCTCTTTAGCGAG	840						
DB	721	TCCGCTCTTAAACAGCAGTGCACACCCCATCAATTACTTCTGTGGGCTCTCTTTAGCGAG	780						
QY	841	CGTCAAATAGCAGAACCTGAAGCTGGTTCTCCAGAGGCTCTGCGAGGACGCGCTGAG	900						
DB	781	CGTCAAATAGCAGAACCTGAAGCTGGTTCTCCAGAGGCTCTGCGAGGACGCGCTGAG	840						
QY	901	GTGGATGAAGGTGGAGGTGGCTTCTCAGGAAACCTTGGAGTGTGCGGAAGCAGATTG	960						
DB	841	GTGGATGAAGGTGGAGGTGGCTTCTCAGGAAACCTTGGAGTGTGCGGAAGCAGATTG	900						
QY	961	GAGCAGTGA	969						
DB	901	GAGCAGTGA	909						

RESULT 13
AAA12208
ID ID AAA12208 standard; cDNA; 969 BP.
XX
AC AAA12208;

XX	11-AUG-2000	(first entry)
DT		
XX	Human G protein-coupled receptor protein cDNA #3.	
DE		
XX	G protein-coupled receptor protein; human; treatment; diagnosis;	
XX	genetic disorder; ss.	
KW		
KW	Homo sapiens.	
OS		
XX	W02000020456-A1.	
PN		
XX	13-APR-2000.	
PD		
XX	30-SEP-1999; 99WO-JP005365.	
XX		
XX	01-OCT-1998; 98JP-00279512.	
PR		
PR	20-OCT-1998; 98JP-00298667.	
XX		
XX	(TAKE) TAKEDA CHEM IND LTD.	
PA		
XX		
XX	Watanabe T, Terao Y, Fukusumi S;	
PI		
XX	WPI; 2000-3033748/26.	
DR		
DR	P-PSDB; AAY87664.	
XX		
XX	Novel human-originated G protein-coupled protein and encoding nucleic	
PT	acid, useful for e.g. identifying ligands and treating diseases	
PT	associated with dysfunction of the protein.	
FT		
XX		
XX	Claim 9; Page 99; 105pp; Japanese.	
PS		
XX		
CC	This invention describes a novel human G protein-coupled receptor protein	
CC	(1). The products of the invention can be used for preventing, treating	
CC	and diagnosing gene diseases and for regulating cellular functions. The	
CC	protein can be used to identify ligands and generate antibodies and	
CC	anistira. It is also useful in the construction of a recombinant receptor	
CC	protein expression system, developing a receptor-binding assay system and	
CC	screening drug candidates and as a probe in diagnosing genetic disorders	
CC	involving G protein-coupled protein. This sequence encodes a human G-	
CC	protein coupled receptor protein described in the method of the invention	
XX	Sequence 969 BP; 179 A; 274 C; 250 G; 266 T; 0 U; 0 Other;	

Query Match	86.5%;	Score	337.8;	DB	3;	Length	969;
Best Local Similarity	91.5%;	Pred. No.	7.8e-226;				
Matches	887;	Conservative	0;	Mismatches	82;	Indels	0;
Matches	887;	Conservative	0;	Mismatches	82;	Indels	0;
QY	1	ATGATTCACCAATCCAGCTCTGGGTACAGAACTGACACCAATCAACAGCAGCTGAGAG	60				
DB	1	ATGATTCACCGTCCAGCTCTGGGTACAAAATGACACCAATCAACAGCAGCTGAGAG	60				
QY	61	ACTCCTTGCTCAAGACAGACCCCTGAGCTTCAGGGGCTGACGTGATCGTGTTCCTTGGTC	120				
DB	61	ACTCCTTGCTCAAGACAGACCCCTGAGCTTCAGGTGCTGAGCTGTCATCATTTCCCTTGGTC	120				
QY	121	CGCTGACAGAAAGCGGTGTGCTCTGGCTCTCTGGCTCCGGCATCCGACGAGGAACGCT	180				
DB	121	GGACTGACAGAAAGCGGTTAGTCTCTGGCTCTCTGGCTCCGGCATCCGACGAGGAACGCT	180				
QY	181	GTCTCCATCTACATCTCAACCTGGTCGCGCGGACTTCCTCTTCCTTAGCGGCCACATT	240				
DB	181	GTCTCCATCTACATCTCAACCTGGCGCGAGCAGACTTCCTCTCCTCAGCTTCAGATT	240				
QY	241	ATATGTTCCGGTTTAGGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCTCT	300				
DB	241	ATACGTTCCGCTTAGGCTCATCAATATCAGCCATCTCATCCGCAAAATCCTCTTTCT	300				
QY	301	GTGATGACCTTTCCCTACTTTTATAGCGCTTAAGCATGTGAGCGCCATCAGCACCCGAGCG	360				
DB	301	GTGATGACCTTTCCCTACTTTTACAGGCTTGATGTGTGAGCGCCATCAGCACCCGAGCG	360				
QY	361	TGCTGTGTCATCTGTGCCCCATCTGGTACCATCTGCCCGGCCCCGAGATCATCTGTCTATCG	420				


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QY 361 TGCCTGTCCTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 420
Db 361 TGCCTGTCCTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 420
QY 421 GTCATGTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 480
Db 421 GTCATGTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 480
QY 481 TGTGATCTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 540
Db 481 TGTGATCTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 540
QY 541 ATCGGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 600
Db 541 ATCGGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 600
QY 601 AGGATCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 660
Db 601 AGGATCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 660
QY 661 ACAGTCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 720
Db 661 ACAGTCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 720
QY 721 AGGATCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 780
Db 721 AGGATCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 780
QY 781 TCCGCTCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 840
Db 781 TCCGCTCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 840
QY 841 CTTCAAAATAGCAGAACTGAACTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 900
Db 841 CTTCAAAATAGCAGAACTGAACTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 900
QY 901 GTGGATGAAGTGGAGGCTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 960
Db 901 GTGGATGAAGTGGAGGCTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 960
QY 961 GAGCAGTGA 969
Db 961 GGGCCATGA 969
```

RESULT 15

```
AAZ10071
ID AAZ10071 standard, DNA; 969 BP.
XX
AC AAZ10071;
XX
XX
DT 20-MAR-2003 (revised)
DT 26-NOV-1999 (first entry)
XX
XX Human dorsal root receptor 5 hDRR5 nucleotide sequence.
XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
KW hDRR5; central nervous system; CNS; anaesthesia; analgesia; neuron;
KW pain. ss.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH 1..969
FT *tag= a
FT /note= "hDRR5"
FT /transl_except= (pos:244..246, aa:Cys)
FT /transl_except= (pos:247..249, aa:Arg)
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FT /transl_except= (pos:445..447, aa:Gly)
FT /transl_except= (pos:448..450, aa:Ser)
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XX WO9932519-A1.
XX 01-JUL-1999.
XX 16-DEC-1998; 98WO-SE002348.
XX 22-DEC-1997; 97SE-00004836.
XX (ASTR ) ASTRA PHARMA INC.
XX (ASTR ) ASTRA AB.
XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
XX WPI; 1999-405162/34.
XX P-PSDB; AAY30363.
XX Rat and human dorsal root receptors and related polynucleotides, useful
XX for identifying agents for anaesthesia and analgesia.
XX Claim 30; Page 59-60; 72pp; English.
XX This is the human dorsal root receptor 5 (hDRR5) nucleotide sequence.
XX hDRR5 is a G protein coupled receptor that is expressed preferentially in
XX dorsal root ganglia. hDRR5 can be used to create antibodies against
XX hDRR5. The dorsal root ganglia area of the central nervous system (CNS)
XX is densely innervated with primary or afferent neurons involved in
XX transmission, modulation and sensation of pain. The DRG's which are
XX expressed in this region of the CNS may be used for assays for the
XX identification of new agents for anaesthesia and analgesia. (Updated on
XX 20-MAR-2003 to correct PA field.)
XX Sequence 969 BP; 179 A; 272 C; 250 G; 268 T; 0 U; 0 Other;
XX
XX Query Match 86.3%; Score 836.2; DB 2; Length 969;
XX Best Local Similarity 91.4%; Pred. No. 2.2e-225;
XX Matches 886; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 1 ATGATTCACCAATCCAGTCTTGGGTACAGAACTGACCAATCAACCGACCTGAGGAG 60
Db 1 ATGATTCACCAATCCAGTCTTGGGTACAGAACTGACCAATCAACCGACCTGAGGAG 60
QY 61 ACTCCTTGTCTACAGACAGACCCCTGAGCTTCACGGGCTGACGTGATCGTTCCCTTGTG 120
Db 61 ACTCCTTGTCTACAGACAGACCCCTGAGCTTCACGGTCTGACGTGATCATTTCCCTTGTG 120
QY 121 CGCTGACAGAAACGGGTTGTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 GGACTGACAGAAACGGGTTGTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GTCTCCATCTACATCTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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QY 241 ATATGTTGCGGTTAGCCTCAATATCCGCTCATCCATCCATCCATCCATCCATCCATCC 300
Db 241 ATATGTTGCGGTTAGCCTCAATATCCGCTCATCCATCCATCCATCCATCCATCCATCC 300
QY 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATCTGAGGCTCATGACGACCGAGCG 360
Db 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATCTGAGGCTCATGACGACCGAGCG 360
QY 361 TGCCTGTCCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 420
Db 361 TGCCTGTCCTCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 420
QY 421 GTCATGTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 480
Db 421 GTCATGTGTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 480
QY 481 TGTGATCTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 540
Db 481 TGTGATCTCCTGTCGCCCCAATCTGGTACCACTGCCCGCCGCCAGATACCTGTCATCG 540
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Qy	541	ATCCGCTGGCTGGT	600
Db	541	GTCCGGTGGCTGGA	600
Qy	601	AGGATTCTCTGTGGATCCCGAAGATGCCGTGACCGAGGTGTACGTGACCATCCTCCTC	660
Db	601	AGGATCCTCTCTGTGGATCCCGAAGATGCCGTGACCGAGGTGTATGTGACCATCCTCCTC	660
Qy	661	ACAGTGTGTCTTCCCTCTGTGGCTGCTGCCCTTGGCATTCAGTGGGCGCTGTTTCC	720
Db	661	ACAGTGTGTCTTCCCTCTGTGGCTGCTGCCCTTGGCATTCAGTGGGCGCTGTTTAC	720
Qy	721	AGGATCCACCTGGATTTGAAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTTCCCTG	780
Db	721	AGGATGCACCTGAATTTGAAAGTCTTATATTGTGATGTGATCTAGTTTCCATTTTCCCTG	780
Qy	781	TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG	840
Db	781	TCCTCTCTAAACAGTAGTGCCACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG	840
Qy	841	CGTCAAAATAGGCAGAACCTGAAGTGTCTCCAGAGGGCTCTGCAGGACACGCCCTGAG	900
Db	841	CGTCAAAATAGGCAGAACCTGAAGTGTCTCCAGAGGGCTCTGCAGGACACGCCCTGAG	900
Qy	901	GTGGATGAAGGTGGAGGGTGGCTTCTCAGGAAACCTCGAGCTGTGCGGAGCAGATTG	960
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Qy	961	GAGCAGTGA	969
Db	961	GGGCCATGA	969

Search completed: July 4, 2004, 05:20:29
Job time : 482 secs

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Sequence 1442, Ap
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Sequence 31, Appl
Sequence 198, App
Sequence 6, Appl
Sequence 51, Appl
Sequence 191, App
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-09-495-050A-164
; Sequence 164, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Roopa, Karl, J.
; APPLICANT: Au-rong, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 164
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 1909132C71
US-09-495-050A-164

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	Query Match	30.0%;	Score 291;	DB 4;	Length 291;
	Best Local Similarity	100.0%;	Pred. No. 7e-73;		
	Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	271	CGCCATCCCATCTCCAAAATCCTCAGTCTCTGTGATGACCTTTCCCTACTTTATAGGCCTA	330		
Db	1	CGCCATCCCATCTCCAAAATCCTCAGTCTCTGTGATGACCTTTCCCTACTTTATAGGCCTA	60		
QY	331	AGCATCTGAGCGCCATCAGCACCGAGCGTGCCTCTCCATCCTGTGGCCCATCTGGTAC	390		
Db	61	AGCATCTGAGCGCCATCAGCACCGAGCGTGCCTCTCCATCCTGTGGCCCATCTGGTAC	120		
QY	391	CATTCGCGCGCCGCCAGATACCTGTATCGTCGCATGTGTCTGTCTGTGGCCCTGTTC	450		
Db	121	CATTCGCGCGCGCCGCCAGATACCTGTATCGTGCATGTGTCTGTCTGTGGCCCTGTTC	180		
QY	451	CTGCTCGGAGTATCTGGATGGATGTTCTGTGACTTCTCTGTTTGTAGTGTGTGATTTCT	510		
Db	181	CTGCTCGGAGTATCTGGATGGATGTTCTGTGACTTCTCTGTTTGTAGTGTGTGATTTCT	240		
QY	511	GTTTGTGTGAACGTCAGATTTTCATTACAAATCGCGTGGCTGTTTTTTTTA	561		
Db	241	GTTTGTGTGAACGTCAGATTTTCATTACAAATCGCGTGGCTGTTTTTTTTA	291		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 05:08:07 ; Search time 94 Seconds
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Perfect score: 969
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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : Issued patents NA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	291	30.0	291	4	US-09-495-050A-164	Sequence 164, App
2	275	28.4	275	4	US-09-016-434-330	Sequence 330, App
3	118.6	12.2	1388	4	US-09-016-434-1255	Sequence 1225, App
4	118.6	12.2	1388	5	PCF-U993-06251-36	Sequence 26, Appl
5	110.8	11.4	2435	5	US-09-484-970B-134	Sequence 134, App
6	96.8	10.0	2416	4	US-09-016-434-1364	Sequence 1264, App
7	94.2	9.7	1327	6	5320941-1	Patent No. 5320941
8	64.4	6.6	136	4	US-09-016-434-210	Sequence 210, App
9	60.6	6.3	7218	1	US-08-232-463-14	Sequence 14, Appl
10	59.2	6.1	2911	3	US-08-981-825-5	Sequence 5, Appl
11	59.2	6.1	2911	3	US-09-480-784-5	Sequence 5, Appl
12	58.4	6.0	2328	4	US-09-016-434-1188	Sequence 1188, App
13	58.4	6.0	2328	4	US-09-023-655-1018	Sequence 1018, App
14	51.6	5.3	263	3	US-09-016-434-327	Sequence 327, App
15	51.6	5.3	265	3	US-08-513-974B-337	Sequence 337, App
16	50	5.2	283	4	US-09-016-434-489	Sequence 489, App
17	49.4	5.1	1002	4	US-09-170-496D-7	Sequence 7, Appl
18	49.4	5.1	1002	4	US-09-170-496D-167	Sequence 167, App
19	49.4	5.1	1285	4	US-09-016-434-1430	Sequence 1430, App
20	48.2	5.0	1866	4	US-09-016-434-1205	Sequence 1205, App
21	47.8	4.9	1285	4	US-09-016-434-1366	Sequence 1366, App
22	47.6	4.9	1875	3	US-09-422-869-21	Sequence 21, Appl
23	47.6	4.9	49136	3	US-09-422-869-1	Sequence 1, Appl
24	46.6	4.8	994	4	US-09-023-655-1082	Sequence 1082, App
25	46.6	4.8	1068	4	US-09-170-496D-129	Sequence 129, App
26	46.4	4.8	1068	4	US-09-170-496D-231	Sequence 231, App
27	46.4	4.8	1161	1	US-08-153-848-31	Sequence 31, Appl

RESULT 2

US-09-016-434-330
; Sequence 330, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 330:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONNUT01
; CLONE: 1909132
; US-09-016-434-330

Query Match 28.4%; Score 275; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.3e-68;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 271 CGCCATCCCATCTCCAAATCCCTCAGTCCTGTGATGACCTTTCCTTACTTTATAGGCCTA 330
DB 1 CGCCATCCCATCTCCAAATCCCTCAGTCCTGTGATGACCTTTCCTTACTTTATAGGCCTA 60
QY 331 AGCATGTGAGCGGCATCAGACCGCGCTGCTGTCATCTCTGTGGCCCATCTGGTAC 390
DB 61 AGCATGTGAGCGGCATCAGACCGCGCTGCTGTCATCTCTGTGGCCCATCTGGTAC 120
QY 391 CACTGCGCGCGCCCGACATACCTGTCTCATGTGTGTCTGTCTGTGGCCCATCTGTCC 450
DB 121 CACTGCGCGCGCCCGACATACCTGTCTCATGTGTGTCTGTCTGTGGCCCATCTGTCC 180
QY 451 CTGTCGGGAGTATCTCTGGAGTGTGATGTCCTGTGACCTCTGTGTAGTGTGTGATCTT 510
DB 181 CTGTCGGGAGTATCTCTGGAGTGTGATGTCCTGTGACCTCTGTGTAGTGTGTGATCTT 240
QY 511 GTTTGGTGTGAACGTGACATTTTCATTACATGCG 545
DB 241 GTTTGGTGTGAACGTGACATTTTCATTACATGCG 275

RESULT 3

US-09-016-434-1225
; Sequence 1225, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1388 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g187388
; US-09-016-434-1225

Query Match 12.2%; Score 118.6; DB 4; Length 1388;
Best Local Similarity 49.6%; Pred. No. 9.3e-24;
Matches 415; Conservative 0; Mismatches 389; Indels 33; Gaps 3;
QY 75 GCAGACCCCTGAGCTTCACGGGGCTGACGTGATCGTTTCCTTGTCCGGCTGACAGGAAA 134
DB 357 GCAAAATCCCATCTGTCACCTGGGTCAATATGAGCATCTCCCGAGTGGGTTTGTGAAA 416
QY 135 CGCGGTTGTGCTCTGGGCTCGCGATCGCAGGAACGCTGTCTCCATCTACAT 194
DB 417 TGGGATTCCTCTGTGTTCTCTGTCTTCGGATGAGAAGAAATCCCTTCACTGTCTACAT 476
QY 195 CTTCAACTGTGTGCGCGCGACTTCCTTCTTCTTAGCGGCCACATTAATATGTTGCGCGTT 254
DB 477 CACCACCCCTGTCTATCGCAGACATCTCACTGCTCTTCTGTATTTTCTGTCTATGGA 536
QY 255 AGCCCTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCTGTGA----- 304
DB 537 CTATGCTTTAGATATAGAGCTTTCTTCTGGCCATTACTACACATTTGACATATCACT 596
QY 305 -----TGACCTTTTCCCTACTTTTATAGCCTTAAGCATGCTGAGCGCCATCAGACCGAGCG 359
DB 597 GACTTTTCTGTTTGGCTACAAACACGGGCTCTATCTGTGACGGCCATTAGTGTGAGAG 656
QY 360 CTGCTGTCCATCTCTGTGGCCCATCTGTGACCATCTGACCTGCGCGCCCGCCAGATACCTGTCTATC 419

Db 657 GTGCTGTCACTCTTTACCCCATCTGTGATCCGATGCCATGCCCAAGTACCAGTGGC 716
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Db 717 ATTGGTCTGTGCCCTCTCTGCTGGCTCTCTCTGCTGGTGTGACCACTGAGTATGTCAT 776
Qy 480 CTGTGACTCTCTGTTTACTGTGCTGATTC-----TGTGTTGGTGTGAACGTGAGATTT 533
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Qy 534 CATTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Db 837 TATAGCCATCTGAGCTTCTGCTGCTTCAAGCCCTCATGCTGCTGCTGCTGCTGCTGCT 896
Qy 594 GCTGCTGAGGATCTCTGCTGATCCCGAAGATCCGCTGATCCAGGCTGTGACGACCAT 653
Db 897 GGTCTGAGATCCGGAAGACACAGTGGCTTCCCATTCCTCCAAAGCTTTACATAGTCAT 956
Qy 654 CTTCTCTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
Db 957 CATGCTCACCATCATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1006
Qy 714 GTTTTCCAGGATCCACCTGATGGAAGTCTTATTTTGTGATGCTGCTGCTGCTGCTGCT 773
Db 1007 --TTTACCTGCTGCTATGATGATTTGCTGACCTTTTGGAACTTACACCAATTTGCT 1064
Qy 774 TTTCTGCTGCTGCTTATACAGAGTGGCAACCCCATCTTACTTCTCTGCTGCTGCTGCT 833
Db 1065 GCTCTTCTCCCAATCAACAGTAGCGCCCAACCTTTTCACTTCTTTTGTGGGAAGCAG 1124
Qy 834 TAGGAGCGCTCAAAATAGGAGGATCCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
Db 1125 TAAGAAGAAGAGATTCAGGAGTCTTAAAGTCTTCTGACCGGGCTTTCAAGA 1181

RESULT 4
PCT-US93-06251-26
; Sequence 26, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; REFERENCE/DOCKET INFORMATION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET INFORMATION: 8586
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1388 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-26
Query Match 12.2%; Score 118.6; DB 5; Length 1388;
Best Local Similarity 49.6%; Pred. No. 9.3e-24;
Matches 415; Conservative 0; Mismatches 389; Indels 33; Gaps 3;
Qy 75 GCAGACCTGAGTTTACCGGGCTGACGTGCAATCGTTTCCCTTGTGCGCTGACAGGAAA 134
Db 357 GCAATCCCATCGTGCACCTGGGTCAATTATGAGCATCTCCCGAGTGGGTTTGTGAGAA 416
Qy 135 CGGGTGTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
Db 417 TGGATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
Qy 195 CTTCAACCTGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
Db 477 CACCCACCTGCTATCGCAGACATCTCACTGCTCTCTGTAATTTTCATCTTGTCTATCGA 536
Qy 255 ACSCCTCAATATCCGGCCATCCCATCTCCAAATTCCTCAGTCTCTGTGA----- 304
Db 537 CTATGCTTTAGATATGAGCTTTCTTCTGGCCATTACTACAAATTTGTACATTATCAGT 596
Qy 305 -----TGACCTTTCCCTACTTTATAGGCTTAAGCATGCTGAGGCCATCAGACCCAGCG 359
Db 597 GACTTTTCTGTTTGGCTACAAACACGGGCTCTATCTGCTGAGGCCATTAGTGTGGAGAG 656
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Qy 714 GTTTTCCAGGATCCACCTGATGGAAGTCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 773
Db 1007 --TTTACCTGCTGCTATGATGATTTGCTGACCTTTTGGAACTTACACCAATTTGCT 1064
Qy 774 TTTCTGCTGCTGCTTATACAGAGTGGCAACCCCATCTTACTTCTCTGCTGCTGCTGCTGCT 833
Db 1065 GCTCTTCTCCCAATCAACAGTAGCGCCCAACCTTTTCACTTCTTTTGTGGGAAGCAG 1124
Qy 834 TAGGAGCGCTCAAAATAGGAGGATCCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
Db 1125 TAAGAAGAAGAGATTCAGGAGTCTTAAAGTCTTCTGACCGGGCTTTCAAGA 1181

RESULT 5
US-09-484-970B-134
; Sequence 134, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.

QY	867	GGTCTCCAGAGGGCTCTCAGACACACGCTGAGGTGGGATGAAGGTGGAGGGTGGGTTCC	936
Db	1411	GGTCTTCCAGCGGGCCCTCGGGACGCGCTGAGCTGGGGGAGGCCGGGGGCAGCCACGC	1470
QY	927	TCAGGAAA	934
Db	1471	CCAACACA	1478
RESULT 6			
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; Sequence 1264, Application US/09016434			
; Patent No. 6500938			
; GENERAL INFORMATION:			
; APPLICANT: Janice Au-Young			
; APPLICANT: Jeffrey J. Seilhamer			
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING			
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION			
; NUMBER OF SEQUENCES: 1490			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.			
; STREET: 3174 PORTER DRIVE			
; CITY: PALO ALTO			
; STATE: CALIFORNIA			
; COUNTRY: USA			
; ZIP: 94304			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/016,434			
; FILING DATE: HEREWITH			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER:			
; FILING DATE:			
; CLASSIFICATION:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Zeller, Karen J.			
; REGISTRATION NUMBER: 37,071			
; REFERENCE/DOCKET NUMBER: PA-0002 US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (650) 855-0555			
; TELEFAX: (650) 845-4166			
; INFORMATION FOR SEQ ID NO: 1264:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 2416 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; IMMEDIATE SOURCE:			
; LIBRARY: GENBANK			
; CLONE: g244209			
; US-09-016-434-1264			

QY 275 ATCCCATCTCCAAATCTCAGTCTGATGACCTTTCCCTACTTTATAGCCCTAAGCA 334
DB 1424 TTTTATCCCTGATTTCTGGCCATATGTCTCCCTTTCTCTTTGAGGTGTCTGTGC 1483
QY 335 TGCTAGGCGCCATCAGCAGCAGCGCTGCTGCTCCATCCTGTGGCCCATCTGGTACCACT 394
DB 1484 TCTGTGTGCTCAGCAGCAGCGCTGCTGCTCCCTCTCTCCCATCTGGTACAGAT 1543
QY 395 GCCGCGCCCGCAGATACCTGTGCTCATCGGTGCTGCTGCTGCTGCGCCCTGCTCCCTGC 454
DB 1544 GCCACCGCCCAAAATACACATCTAATGTTGCTGACCCCTCATCTGGGGCTGCTCTTTT 1603
QY 455 TGCGAGTATCTCGAGTGGATGTTCTGTGACTTCTCTGTTTGTAGTGTCTGATTTCTGTT 514
DB 1604 GCATCAACATAGTAAATACATTTTCTTAACTTACTGGAACATGTAAAGCATGTGTCA 1663
QY 515 GGTGTGAACGTCAGATTTCAATCAATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
DB 1664 TATTTCTAAAG-----CTTCTGGGCTCTTCCATGCTATCTTCACTTGTGATGT 1714
QY 575 GTGGTCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
DB 1715 GTGTGCTGAGTCTGACTCTACTCACTTAGATTCCTGTGCTGCTGCTGCTGCTGCTGCT 1774
QY 635 CCAGCTGTAGTGAACATCTCTCCTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 694
DB 1775 CCAGGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1834
QY 695 TTGGGATTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754
DB 1835 TGAGC-----GTGGACCCCTCATTAACAGATTCGAAATGTTGTGCTCA 1879
QY 755 ATGTGCACTAGTTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814
DB 1880 CCTCCTATTATTTCTGTTTCTCT---CATTTAAACAGCAGCGCCCAACCTATCACTT 1936
QY 815 ACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 874
DB 1937 ATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1996
QY 875 AGAGGCTCTGAGGACACGCTGAGGTGG 904
DB 1997 AACGGCGTTAGCAGATAGCAGAGGTGG 2026

RESULT 7

5320941-1
; Patent No. 5320941
; Applicant: Young, Dallen; Wigler, Michael H.; Fasano
; Ottavio
; TITLE OF INVENTION: DNA SEQUENCES ENCODING MAS ONHCOGENE,
; POLYPEPTIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHODS
; BASED THEREFROM
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/872,087
; FILING DATE: 06-JUN-1986
; SEQ ID NO: 1:
; LENGTH: 1327
5320941-1

Query Match 9.7%; Score 94.2; DB 6; Length 1327;
Best Local Similarity 48.5%; Pred. No. 7.3e-17;
Matches 338; Conservative 0; Mismatches 338; Indels 21; Gaps 2;

QY 75 GCAGACCTCTGAGCTTACGCGGCTGACGTGCTATCGTTTCCCTGCGCTGACAGGAAA 134
DB 356 GCAATCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
QY 135 CGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 194
DB 416 TGGGATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475

QY 195 CCTCAACCTGGTCCGCGCGACTTCTCTTCTTAGCGGCCACATATATGTTGCGCGTT 254
DB 476 CACCCACCTGTCTATCGCAGACATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 535
QY 255 ACSCCTCATCATATCCGCCATCCCATCTCCAAATCTCAGTCTCTGTA----- 304
DB 536 CTATGCTTTAGATTTAGAGCTTTCTTCTGGCCATTTACTACAAATTTGTCACATTTACGT 595
QY 305 -----TGACCTTTCCCTACTTTTATAGCCCTAAGCATGCTGAGCGCCATCAGCACCGAGCG 359
DB 596 GAGTTTCTGTTTGGCTACAAACAGGCGCTCTATCTGCTGACGGCCATTTAGTGTGAGAG 655
QY 360 CTGCTGTCTCATCTGCGCCATCTGTTACCACTGCGCGCCCGCCCGCCAGATACCTGTGATC 419
DB 656 GTGCTGTGCTGCTGCTTACCCCATCTGTTACCCATCTGTTACCCATCTGCGCCATCGCC 715
QY 420 GGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479
DB 716 ATTGGTCTGCGCCCTTCTGTTGGCTCTTCTGTTGGTGTGACCATGAGTATGTCAT 775
QY 480 CTGTGACTTC-----CTGTTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
DB 776 GTGATCCACACAGAAAGAGAGTGAATCTCCGAATGACTGCCACAGCTCATCATCTT 835
QY 534 CATTACATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
DB 836 TATAGCATCTCTGAGCTTCTGTTGCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 594 GCTGGTCAAGATCTCTGTTGATCCCGAGATGCGCTGACAGCGCTGTACGTGACCAT 653
DB 896 GGTGCTGAGATCCCGAGAAACAGTGGGCTTCCCATTCCTCAAGCTTTACATAGTCAT 955
QY 654 CTCTCTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
DB 956 CATGGTCAACCATATTATCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015
QY 714 GTTTTCCAGGATCCACTGATTTGAAAGTCTTATTT 750
DB 1016 GTACTACAGTAGCGCAACCCCTTCTTACTTCTTT 1052

RESULT 8

US-09-016-434-210
; Sequence 210, Application US/09016434
; Patent No. 650938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT07
; CLONE: 1506560
; US-09-016-434-210

Query Match 6.6%; Score 64.4; DB 4; Length 196;
Best Local Similarity 63.6%; Pred. No. 7.7e-09;
Matches 98; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 350 GCACCGAGCGCTGCTGTCATCTGCTGCGCCATCTGGTACCACTGCGCGCCCGCCAGAT 409
Db 1 GCACCGAGCGCTGCGCTGCTGCTGCGCCATCTGGTACCACTGCGCGCCCGCCAGAT 409

QY 410 ACCTGTCATCGGTGCTGCTGCTGCTGCGCCCTGCTGCTGCGCGAGTATCCTGG 469
Db 61 GCCTGTCGCGCGTGGTGGCGCTGCTGCTGCGCGAGTATCCTGG 469

QY 470 AGTGGATGTTCTGTGACTTCTGTTAGTGTGTC 503
Db 121 ACAACTACTTCTGCTGTTCTGCGCGCGCGGCG 154

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT29pt-F1s
; US-08-232-463-14

Query Match 6.3%; Score 60.6; DB 1; Length 7218;
Best Local Similarity 4.5%; Pred. No. 5.4e-07;
Matches 18; Conservative 228; Mismatches 157; Indels 0; Gaps 0;

QY 136 CGCGTTGTGCTCGCTCGGCTGCGGATGCGGATGCGGAGGAGCGTCTCATCATCATC 195
Db 1056 GAGCTTCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1115

QY 196 CTCACCTGTCGCGCGCGGCTGCTGCTGCTGAGCGGCACATATATATGTCGCCGTTA 255
Db 1116 YVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1175

QY 256 CGCCTCATCATATCCGCCATCCCATCTCCAAATCTCAGTCTGATGACCTTTCCC 315
Db 1176 YVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1235

QY 316 TACTTTATAGCTTAAGCATGCTGAGCGCCATCAGCAGCGCTGCTGCTGCTGCTG 375
Db 1236 YVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1295

QY 376 TGGCCCATCTGTTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 435
Db 1296 YVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1355

QY 436 CTCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
Db 1356 YVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1415

QY 496 AGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 538
Db 1416 YVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV 1458

RESULT 10
US-08-981-825-5
; Sequence 5, Application US/08981825
; Patent No. 6040426
; GENERAL INFORMATION:
; APPLICANT: OGAWA, KAZUYAUKI
; APPLICANT: TANAKA, KAZUYA
; APPLICANT: NAGATA, KINYA
; APPLICANT: TAKANO, SYOICHI
; TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
; NUMBER OF SEQUENCES: 6
; NUMBER OF INVENTION: Th2, GENE (B19) ENCODING THE SAME, AND
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,825
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
```

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/
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: MSHIM4.001APC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 714-760-0404
/ TELEFAX: 714-760-9502
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2911 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: unknown
/ MOLECULE TYPE: CDNA
/ US-08-981-825-5

Query Match 6.1%; Score 59.2; DB 3; Length 2911;
Best Local Similarity 48.8%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 198; Indels 12; Gaps 1;

Qy 96 GGTGACGTCATCGTTTCCCTTGTGCGCTGACAGAAACGGGTTGTGCTCTGGCTCCT 155
Db 223 GCTGACGGGCTGGCTCGCTGCGGCTGGTGAGAAATGGAGTCATCTCTTCGTGGT 282

Qy 156 GGGCTGCGCATGCGCAGAACGCTGCTCCATCTACATCTCACTGCTGCGGCCGA 215
Db 283 GGGCTGCGCATGCGCAGAACGCTGCTCCATCTACATCTCACTGCTGCGGCCGA 342

Qy 216 CTTCTCT-----CTTCTTAGCGGCCACATTATATGTTTCGCCGTTACGCTCAT 263
Db 343 CTTCTTAGCGGCCACATTATATGTTTCGCCGTTACGCTCAT 402

Qy 264 CAATATCGGCATCCATCTCAAAATCTCTAGTCTGTGATGACCTTCCCTACTTTAT 323
Db 403 GGAGCTGGGCACACCTTCTGAAACTGACCTCTCCATCTTCTTCTCAACATGTTCCG 462

Qy 324 AGGCCTAAGCATGCTGAGCGCCATCAGACCGAGCGCTGCTGCTCCATCTCTGCGCCAT 383
Db 463 CAGCGGCTTCTGCTCAGCGCCATCAGCGCTGAGCGCTGCTGCTGCGCGGCT 522

Qy 384 CTGTACACTGCGCGCGCCCGCCAGATACCTGTCTCATCGGTGATGTTCTGCTCTGGGC 443
Db 523 GTGGGCGCAGAACCCACCGCCCGCGCGCCGCGCCGCGCGCGCGCGCGG 582

Qy 444 CTTGTCCTCTGCGGAGTATCTTGGAGTGATGTTCTGCTGACTTCTCTGT 493
Db 583 ACTAGCGGTGCTCAACACGGTGCCTTATTTCTGTTCCGGGACACCATCT 632

RESULT 11
US-09-480-784-5
Sequence 5, Application US/09480784
Patent No. 6156186
GENERAL INFORMATION:
APPLICANT: OGAWA, KAZUYAUKI
TANAKA, KAZUYA
TAKANO, KYOICHI
TAKANO, SYOICHI
TITLE OF INVENTION: Th2, GENE (B19) ENCODING THE SAME, AND
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

/
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: MSHIM4.001APC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 714-760-0404
/ TELEFAX: 714-760-9502
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2911 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: unknown
/ MOLECULE TYPE: CDNA
/ US-08-981-825-5

Query Match 6.1%; Score 59.2; DB 3; Length 2911;
Best Local Similarity 48.8%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 198; Indels 12; Gaps 1;

Qy 96 GGTGACGTCATCGTTTCCCTTGTGCGCTGACAGAAACGGGTTGTGCTCTGGCTCCT 155
Db 223 GCTGACGGGCTGGCTCGCTGCGGCTGGTGAGAAATGGAGTCATCTCTTCGTGGT 282

Qy 156 GGGCTGCGCATGCGCAGAACGCTGCTCCATCTACATCTCACTGCTGCGGCCGA 215
Db 283 GGGCTGCGCATGCGCAGAACGCTGCTCCATCTACATCTCACTGCTGCGGCCGA 342

Qy 216 CTTCTCT-----CTTCTTAGCGGCCACATTATATGTTTCGCCGTTACGCTCAT 263
Db 343 CTTCTTAGCGGCCACATTATATGTTTCGCCGTTACGCTCAT 402

Qy 264 CAATATCGGCATCCATCTCAAAATCTCTAGTCTGTGATGACCTTCCCTACTTTAT 323
Db 403 GGAGCTGGGCACACCTTCTGAAACTGACCTCTCCATCTTCTTCTCAACATGTTCCG 462

Qy 324 AGGCCTAAGCATGCTGAGCGCCATCAGACCGAGCGCTGCTGCTCCATCTCTGCGCCAT 383
Db 463 CAGCGGCTTCTGCTCAGCGCCATCAGCGCTGAGCGCTGCTGCTGCGCGGCT 522

Qy 384 CTGTACACTGCGCGCGCCCGCCAGATACCTGTCTCATCGGTGATGTTCTGCTCTGGGC 443
Db 523 GTGGGCGCAGAACCCACCGCCCGCGCGCCGCGCGCGCGCGCGCGG 582

Qy 444 CTTGTCCTCTGCGGAGTATCTTGGAGTGATGTTCTGCTGACTTCTCTGT 493
Db 583 ACTAGCGGTGCTCAACACGGTGCCTTATTTCTGTTCCGGGACACCATCT 632

RESULT 12
US-09-016-434-1188
Sequence 1188, Application US/09016434
Patent No. 6509338
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 FORSTER DRIVE
```


Db 521 TGCTGACCATACCTCTCTCTCTGACCGGTGGTCCGG 558

RESULT 14
US-09-016-434-327
; Sequence 327, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 327:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT07
; CLONE: 1889801

US-09-016-434-327

Query Match 5.3%; Score 51.6; DB 4; Length 263;
Best Local Similarity 62.3%; Pred. No. 3.7e-05;
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 107 TCGTTTCCCTTCTGCGGTGACAGGAACGCGTGTGTGCTCTGGCTCTGGGCTCCGCCA 166
Db 54 TCTCTGCTCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 113
QY 167 TGGGAGGAGCGTGTCTGTCTCATCTACATCTCAACCTGTCCGCGCGCATCTCTCTTCC 226
Db 114 TCAAGAGGAGCGCTTCTCTCATCTACTTCTGCACTGTCCGCGCGCATGTGGGCTACC 173
QY 227 TTAGCGGCCA 236
Db 174 TCTTCAGCAA 183

RESULT 15
US-08-513-974B-337
; Sequence 337, Application US/08513974B
; Patent No. 6114139

GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, SYO
; APPLICANT: Chitaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ogi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 337:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA


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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..264
US-08-513-974B-337

Query Match      5.3%; Score 51.6; DB 3; Length 265;
Best Local Similarity 56.5%; Pred. No. 3.7e-05;
Matches 96; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY      118  GTCGGCTGACAGGAAACCGGTTGTGCTCGCTCCTGGGCTGCGGATGCGGAGGAC 177
Db      1   GTGGGCATGGTGGGCAACGTGTGCTCTGCTTCTCGGTTCTCCATCAAGAGGACC 60

QY      178  GCTGTCTCCATCTACATCCTCAACCTGTGTCGGGGCGGACTTCCTCTTCTTAGCGGCCAC 237
Db      61  CCCTTCTCCGCTCTACTTCTGACCTGGCCAGCGCGGCGGCTACCTCTTCAGCAAG 120

QY      238  ATTATATGTTCCCGGTTACGCTCATCAATATCCGGCATCCCATCTCCAA 287
Db      121  GCCGTGTTCTCCTGCTGTAACGCGGGCGGCTTCCTGGGCACCTTCGCCCA 170
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Search completed: July 4, 2004, 07:23:24
Job time : 97 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 06:30:08 ; Search time 525 Seconds
(without alignments)

8904.109 Million cell updates/sec

Title: US-09-787-879C-3

Perfect score: 969

Sequence: 1 atggattcaaccatccagct.....gaagcagattggagcagtga 969

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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1: /cgn2_6/ptodata/2/pubnpa/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubnpa/FCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubnpa/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubnpa/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubnpa/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubnpa/FCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	969	100.0	969	9	US-09-995-225-19
2	969	100.0	969	10	US-09-995-225-19
3	969	100.0	1400	15	US-10-183-116-30
4	969	100.0	1400	15	US-10-225-567A-673
5	969	100.0	2618	12	US-09-867-570-1
6	969	100.0	8622	12	US-09-867-570-3
7	965.8	99.7	969	13	US-10-401-397A-1
8	965.8	99.7	1369	16	US-10-292-798-1273
9	964.2	99.5	969	13	US-10-391-074-1
10	845.8	87.3	909	15	US-10-237-467-9
11	833	86.0	969	9	US-09-995-225-17
12	833	86.0	969	10	US-09-995-225-17
13	833	86.0	969	15	US-10-237-467-3
14	833	86.0	1369	16	US-10-292-798-1041

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15 833 86.0 1604 15 US-10-183-116-32 Sequence 32, Appl
16 833 86.0 1604 15 US-10-225-567A-688 Sequence 688, App
17 829.8 85.6 969 13 US-10-343-650A-43 Sequence 43, Appl
18 829.8 85.6 969 15 US-10-079-384-3 Sequence 3, Appli
19 829.8 85.6 969 15 US-10-240-998-3 Sequence 3, Appli
20 829.8 85.6 969 15 US-10-321-807-19 Sequence 19, Appl
21 829.8 85.6 969 15 US-10-237-467-11 Sequence 11, Appl
22 829.8 85.6 969 13 US-10-072-012-171 Sequence 171, App
23 829.8 85.6 969 13 US-10-072-012-171 Sequence 171, App
24 829.8 85.6 1369 16 US-10-017-161-1055 Sequence 1055, Ap
25 829.8 85.6 1369 16 US-10-292-798-897 Sequence 897, App
26 829.8 85.6 1369 16 US-10-183-116-15 Sequence 15, Appl
27 829.8 85.6 1370 15 US-10-017-161-1599 Sequence 1599, Ap
28 829.8 85.6 1370 15 US-10-072-012-173 Sequence 173, App
29 829.8 85.6 1370 15 US-10-072-012-173 Sequence 173, App
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31 792.2 81.8 966 15 US-10-240-998-6 Sequence 6, Appli
32 764.2 78.9 994 13 US-10-072-012-169 Sequence 169, App
33 729.4 75.3 1369 16 US-10-219-834-7 Sequence 7, Appli
34 697.4 72.0 969 15 US-10-101-510-239 Sequence 239, App
35 618.8 63.9 961 15 US-10-240-998-7 Sequence 7, Appli
36 596.6 61.6 1003 10 US-09-800-321A-30 Sequence 30, Appl
37 596.6 61.6 1030 13 US-10-072-012-175 Sequence 175, App
38 587.2 60.6 994 15 US-10-240-998-8 Sequence 8, Appli
39 587.2 60.6 1163 9 US-09-750-373-11 Sequence 11, Appl
40 587.2 60.6 1300 15 US-10-183-116-17 Sequence 17, Appl
41 587.2 60.6 1300 15 US-10-225-567A-648 Sequence 648, App
42 587.2 60.6 1393 15 US-10-017-161-1053 Sequence 1053, App
43 587.2 60.6 1393 16 US-10-292-798-895 Sequence 895, App
44 587.2 60.6 1394 16 US-10-292-798-1269 Sequence 1269, Ap
45 587.2 60.6 1770 9 US-09-920-068A-8 Sequence 8, Appli
45 585.8 60.5 993 9 US-09-826-508-11 Sequence 11, Appl
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ALIGNMENTS

RESULT 1

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US-09-995-225-19
; Sequence 19, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
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;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 19
;; LENGTH: 969
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-19

Query Match 100.0%; Score 969; DB 9; Length 969;
Best Local Similarity 100.0%; Pred. No. 1.2e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
Db 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60

QY 61 ATCTCTTGCTACAGAGACCTTGAGCTTCAAGGGGCTGACGTGATCGTTCCCTTGTG 120
Db 61 ATCTCTTGCTACAGAGACCTTGAGCTTCAAGGGGCTGACGTGATCGTTCCCTTGTG 120

QY 121 GCGCTGACAGGAACCGGTGTGCTCTGGCTCTGGGCTGCGGATGCGGAGGACGCT 180
Db 121 GCGCTGACAGGAACCGGTGTGCTCTGGCTCTGGGCTGCGGATGCGGAGGACGCT 180

QY 181 GTCTCCATCTACATCCTCAACCTGTGTGCGGCGGACTTCTCTTCTTACGCGCCACAT 240
Db 181 GTCTCCATCTACATCCTCAACCTGTGTGCGGCGGACTTCTCTTCTTACGCGCCACAT 240

QY 241 ATATGTCGCGGTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCT 300
Db 241 ATATGTCGCGGTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCT 300

QY 301 GTGATGACCTTCCCTACTTTATAGGCTAAGCATCTGAGCGCCATCAGACCGAGCGC 360
Db 301 GTGATGACCTTCCCTACTTTATAGGCTAAGCATCTGAGCGCCATCAGACCGAGCGC 360

QY 361 TGCTGTCCATCTGTGGCCCATCTGTATACATCTGCGCGCCGCGGATACCTGTTCATCG 420
Db 361 TGCTGTCCATCTGTGGCCCATCTGTATACATCTGCGCGCCGCGGATACCTGTTCATCG 420

QY 421 GTCATGTGTCTCTGCTCTGGGCTCTCTCTGCTGCGGAGTATCTCTGAGTGGATGTT 480
Db 421 GTCATGTGTCTCTGCTCTGGGCTCTCTCTGCTGCGGAGTATCTCTGAGTGGATGTT 480

QY 481 TGTGACTTCTCTGTTAGTGTGTGATCTGTTGTGTGTAACGTCAGATTTCATTACA 540
Db 481 TGTGACTTCTCTGTTAGTGTGTGATCTGTTGTGTGTAACGTCAGATTTCATTACA 540

QY 541 ATCCGCTGGCTGTTTCTTTTATGTGTGTTCTCTGTGGCTCCAGCCTGGTCTGCTGTC 600
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QY 601 AGGATCTCTGTGATCCCGAAGATCCCGTGTACAGGCTGTACGTGACCATCTCTCTC 660
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QY 781 TCCGCTCTTACAGAGTGCACCGCATCTTCTTCTTCTGCGGCTCTCTTATGCGAG 840
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QY 841 CGTCAAAATAGGAGACCTGAAGCTGTGTTCTCCAGAGGGCTCTGACGACACGCTGAG 900

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Db 961 GAGCAGTGA 969

RESULT 2
US-09-995-225-19
; Sequence 19, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 03/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-19

Query Match 100.0%; Score 969; DB 10; Length 969;
Best Local Similarity 100.0%; Pred. No. 1.2e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
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QY 61 ACTCTCTGTCTACAGAGACCTTGAGCTTCAAGGGGCTGAGCTGATCGTTCCCTTGTG 120
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Db GCGTGCAGAGAAACGGTGTGTCTCTGGCTCTCTGGCTCGCGCATCGCAGAAACGCT 180
181 GTCTCCATCTACATCCTCAACCTGTGTGCGGCGCAGATTCCTCTCTCTAGGGGCAACATT 240
Db GTCTCCATCTACATCCTCAACCTGTGTGCGGCGCAGATTCCTCTCTCTAGGGGCAACATT 240
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Db TGCCTGTCCATCTCTGCGCCCATCTGTTACACATGCGCGCCGCGCATCTGTCATCG 420
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661 ACAGTGTCTGCTCTCTCTCTCTCTGCGCTGCGCTTGGCATTCAGTGGCGCTCTGTTTCC 720
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Db AGGATCCACTGGATGGAAAGTCTTATTTTGTGATGTGATCTAGTTTCATTTTCTG 780
781 TCGCTCTTAACAGCAGTGCACCCCATCTTCTCTGCTGCGCTCTCTTCTGCTGCTTCTAGGCAG 840
Db TCGCTCTTAACAGCAGTGCACCCCATCTTCTCTGCTGCGCTCTCTTCTGCTGCTTCTAGGCAG 840
841 CGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGCTCTGCAGACACGCTGAG 900
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901 GTGGATGAAGTGGAGGCTGCTCTCAGGAAACCTGAGCTGTGCGGAGCAGATTG 960
Db GTGGATGAAGTGGAGGCTGCTCTCAGGAAACCTGAGCTGTGCGGAGCAGATTG 960
961 GAGCAGTGA 969
Db GAGCAGTGA 969

RESULT 3
US-10-183-116-30
; Sequence 30, Application US/10183116
; Publication No. US2003092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI

CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (332)...(1297)
US-10-183-116-30
Query Match 100.0%; Score 969; DB 15; Length 1400;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGATTCAACCATCCCGAGTCTTGGGTACAGAACTGACACCAATCAACGACGCTGAGGAG 60
Db 332 ATGGATTCAACCATCCCGAGTCTTGGGTACAGAACTGACACCAATCAACGACGCTGAGGAG 391
QY 61 ACTCCTTGTCTACAGCAGACCCCTGAGCTTCAACGGGCTGACGTGCTATCGTTCCCTTGTG 120
Db 392 ACTCCTTGTCTACAGCAGACCCCTGAGCTTCAACGGGCTGACGTGCTATCGTTCCCTTGTG 451
QY 121 GCGTGCAGAGAAACGGTGTGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 180
Db 452 GCGTGCAGAGAAACGGTGTGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 511
QY 181 GTCTCCATCTACATCCTCAACCTGCTGCGGCGCATCTTCTCTCTTCTTACGCGCCACATT 240
Db 512 GTCTCCATCTACATCCTCAACCTGCTGCGGCGCATCTTCTCTCTTCTTACGCGCCACATT 571
QY 241 ATATGTTTGGCGCTTACGCTTCATCAATATCCGCCATCCCATCTCCAAATTCCTCAGTCCT 300
Db 572 ATATGTTTGGCGCTTACGCTTCATCAATATCCGCCATCCCATCTCCAAATTCCTCAGTCCT 631
QY 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGACACGAGCGC 360
Db 632 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGACACGAGCGC 691
QY 361 TGCCTGTCCATCTCTGTTGGCCCATCTGTTACCACTGCGCGCCGCGCCAGATACCTGTCTATCG 420
Db 692 TGCCTGTCCATCTCTGTTGGCCCATCTGTTACCACTGCGCGCCGCGCCAGATACCTGTCTATCG 751
QY 421 GTCATGTGTCTCTGCTCTGCGCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 752 GTCATGTGTCTCTGCTCTGCGCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
QY 481 TGTGACTTCTCTTTAGTGGTGTGATTTCTGTTGGTGTGAAAGTCAAGATTCATTACA 540
Db 812 TGTGACTTCTCTTTAGTGGTGTGATTTCTGTTGGTGTGAAAGTCAAGATTCATTACA 871
QY 541 ATCGCGTGGCTGTTTTTATGTTGTTCTCTGTTGGTCTCAGCTGAGCCTCTGCTGCTGCTGCTGCT 600
Db 872 ATCGCGTGGCTGTTTTTATGTTGTTCTCTGTTGGTCTCAGCTGAGCCTCTGCTGCTGCTGCTGCT 931
QY 601 AGGATTTCTGTGGATCCCGGAAGATGCGGTGACACAGGCTGTACGTGACCATCTCTCTC 660
Db 932 AGGATTTCTGTGGATCCCGGAAGATGCGGTGACACAGGCTGTACGTGACCATCTCTCTC 991
QY 661 ACAGTGTGCTTCTCTCTCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

LOCATION: (201)...(1169)
US-10-292-798-1273

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Query Match      99.7%; Score 965.8; DB 16; Length 1369;
Best Local Similarity 99.6%; Pred. No. 1.4e-290;
Matches 967; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 60
DB 201 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 260
QY 61 ACTCCTTGTACAGAGACCCCTGAGCTTACGCGGCTGACGTGATGTTCCCTTGTTC 120
DB 261 ACTCCTTGTACAGAGACCCCTGAGCTTACGCGGCTGACGTGATGTTCCCTTGTTC 320
QY 121 GGGCTGACAGGAAAGCGGCTTGTGCTCTGGCTCCCTGGCTGCGCATGCGAGGAACGCT 180
DB 321 GCGCTGACAGGAAAGCGGCTTGTGCTCTGGCTCCCTGGCTGCGCATGCGAGGAACGCT 380
QY 181 GTCTCATCTACATCTCAACTGCTGAGCTGCGGCGGCTTCTCTTCTTAGCGGCACATT 240
DB 381 GTCTCATCTACATCTCAACTGCTGAGCTGCGGCGGCTTCTCTTCTTAGCGGCACATT 440
QY 241 ATATGTTCCCGCTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
DB 441 ATATGTTCCCGCTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 500
QY 301 GTGATGACCTTTCCTTACCTTTATAGCTTAAGCTAAGCTGAGCGGCATCAGACCGAGCGC 360
DB 501 GTGATGACCTTTCCTTACCTTTATAGCTTAAGCTAAGCTGAGCGGCATCAGACCGAGCGC 560
QY 361 TGCCTGTCCATCTGTGGGCCATCTGGTACCACTGCGCGGCCCGAGATACCTGTCACTCG 420
DB 561 TGCCTGTCCATCTGTGGGCCATCTGGTACCACTGCGCGGCCCGAGATACCTGTCACTCG 620
QY 421 GTCATGTGTCTGTCTGTGGCCCTGTCTGTCTGTGGCTGCGGAGTATCTGTGAGTGTTC 480
DB 621 GTCATGTGTCTGTCTGTGGCCCTGTCTGTCTGTGGCTGCGGAGTATCTGTGAGTGTTC 680
QY 481 TGTGACTTCTCTTGTAGTGGTCTGATCTGTTGGTGTGGTGAACGTTCAGATTTCATTACA 540
DB 681 TGTGACTTCTCTTGTAGTGGTCTGATCTGTTGGTGTGGTGAACGTTCAGATTTCATTACA 740
QY 541 ATCGCGTGGCTGTTTATTTATGTGTGTCTCTGTGGTCCAGCGCTGTCTGTCTGTCTG 600
DB 741 ATCGCGTGGCTGTTTATTTATGTGTGTCTCTGTGGTCCAGCGCTGTCTGTCTGTCTG 800
QY 601 AGGATCTCTGTGGATCCCGGAGATGCGCTGACAGAGCTGTAGTACCACTCTCTCTC 660
DB 801 AGGATCTCTGTGGATCCCGGAGATGCGCTGACAGAGCTGTAGTACCACTCTCTCTC 860
QY 661 ACAGTCTGTCTCTCTCTGTGGCTGCGCTTGGCATTCAGTGGGCGCTGTTTTC 720
DB 861 ACAGTCTGTCTCTCTCTGTGGCTGCGCTTGGCATTCAGTGGGCGCTGTTTTC 920
QY 721 AGGATCCACTGATTTGGAAGTCTTATTTGTGATGCTACTAGTTCATTTTCTCTG 780
DB 921 AGGATCCACTGATTTGGAAGTCTTATTTGTGATGCTACTAGTTCATTTTCTCTG 980
QY 781 TCCGCTCTTAAACAGAGAGTGCACCCCATCATTTACTTCTCTGTGGCTCTTTTAGGCG 840
DB 981 TCCGCTCTTAAACAGAGAGTGCACCCCATCATTTACTTCTCTGTGGCTCTTTTAGGCG 1040
QY 841 CGTCAAAATAGGAGAACTGAGCTGTTCTCCAGAGGCTCTGACAGACACGCTGAG 900
DB 1041 CGTCAAAATAGGAGAACTGAGCTGTTCTCCAGAGGCTCTGACAGACACGCTGAG 1100
QY 901 GTGATGAGAGTGGAGGTGGCTTCTCTCAGGAAACCTCGAGCTGTGCGGAGAGCATTTG 960
DB 1101 GTGATGAGAGTGGAGGTGGCTTCTCTCAGGAAACCTCGAGCTGTGCGGAGAGCATTTG 1160
QY 961 GAGCAGTGA 969
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DB 1161 GAGCAGTGA 1169

RESULT 9
US-10-391-074-1
; Sequence 1, Application US/10391074
; Publication No. US20040038345A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael
; APPLICANT: Wattler, Frank
; TITLE OF INVENTION: No. US20040038345A1e1 Human Seven-Transmembrane Receptors
; FILE REFERENCE: 7705.0008-00-000
; CURRENT APPLICATION NUMBER: US/10/391,074
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-391-074-1

Query Match      99.5%; Score 964.2; DB 13; Length 969;
Best Local Similarity 99.7%; Pred. No. 3.9e-290;
Matches 966; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 60
DB 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 60
QY 61 ACTCCTTGTCTACAGAGACCCCTGAGCTTCAAGGCTGACGTGATGTTCCCTTGTTC 120
DB 61 ACTCCTTGTCTACAGAGACCCCTGAGCTTCAAGGCTGACGTGATGTTCCCTTGTTC 120
QY 121 GCGTGTACAGAGAAAGCGGCTTGTCTGTCTGTGGCTGCGGAGTATGCGAGAAAGCT 180
DB 121 GCGTGTACAGAGAAAGCGGCTTGTCTGTCTGTGGCTGCGGAGTATGCGAGAAAGCT 180
QY 181 GTCTCCATCTACATCTCTCAACCTGCTGCGGCGGCTGACGTGATGTTCCCTTGTTC 240
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QY 241 ATATGTTGGCGGTGAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
DB 241 ATATGTTGGCGGTGAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
QY 301 GTGATGACCTTTCCTTACTTTATAGGCTTAAGCATGCTGAGCGCCATCAGACCGAGCGC 360
DB 301 GTGATGACCTTTCCTTACTTTATAGGCTTAAGCATGCTGAGCGCCATCAGACCGAGCGC 360
QY 361 TGCCTGTCCATCTCTGTGGCCCATCTGTGTACCACTGCGCGGCCCGCCAGATACCTGTCT 420
DB 361 TGCCTGTCCATCTCTGTGGCCCATCTGTGTACCACTGCGCGGCCCGCCAGATACCTGTCT 420
QY 421 GTCATGTGTCTCTGTCTGCGCCCTGTCTCTCTGCGGAGTATCTGAGAGTGAATGTC 480
DB 421 GTCATGTGTCTCTGTCTGCGCCCTGTCTCTCTGCGGAGTATCTGAGAGTGAATGTC 480
QY 481 TGTGACTTCTCTTGTAGTGGTGTGATTTCTTGTGTGTGAAACGTGAGATTTTCAATACA 540
DB 481 TGTGACTTCTCTTGTAGTGGTGTGATTTCTTGTGTGTGAAACGTGAGATTTTCAATACA 540
QY 541 ATCCGCTGGCTGTTTTTTTATGTGTGGTCTCTGTGGGTCCAGCTGGTCTGTCTGTC 600
DB 541 ATCCGCTGGCTGTTTTTTTATGTGTGGTCTCTGTGGGTCCAGCTGGTCTGTCTGTC 600
QY 601 AGGATTTCTGTGTGATCCCGGAGATGCGCTGACAGAGCTGTACGTGACCACTCTCTC 660
DB 601 AGGATTTCTGTGTGATCCCGGAGATGCGCTGACAGAGCTGTACGTGACCACTCTCTC 660
QY 661 ACAGTGTGTCTTCTCTCTGTGGCTCTGTGGCTCTGTGGCTCTGTGGCTCTGTGGCTCT 720
DB 661 ACAGTGTGTCTTCTCTCTGTGGCTCTGTGGCTCTGTGGCTCTGTGGCTCTGTGGCTCT 720
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QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTCATTTCCCTG 780
Db 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTCATTTCCCTG 780
QY 781 TCCGCTCTTAACAGCAGTGGCAACCCCATCATTTACTTCTTGTGGGCTCTTTTAGGCAG 840
Db 781 TCCGCTCTTAACAGCAGTGGCAACCCCATCATTTACTTCTTGTGGGCTCTTTAGGCAG 840
QY 841 CGTCAAAATAGGCGAAGACCTGAAGCTGGTCTCCAGAGGCTCTGAGGACAGCCTGAG 900
Db 841 CGTCAAAATAGGCGAAGACCTGAAGCTGGTCTCCAGAGGCTCTGAGGACAGCCTGAG 900
QY 901 GTGGATGAAGTGGAGGCTGGCTTCCCTCAGAAACCTGGAGCTGTCCGGAACAGATTG 960
Db 901 GTGGATGAAGTGGAGGCTGGCTTCCCTCAGAAACCTGGAGCTGTCCGGAACAGATTG 960
QY 961 GAGCAGTGA 969
Db 961 GAGCAGTGA 969

RESULT 10
US-10-237-467-9
; Sequence 9, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Jiayu
; APPLICANT: Gray, Nathanael S.
; APPLICANT: Caldwell, Jeremy C.
; APPLICANT: Schultz, Peter G.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Sensory Neuron Receptors
; FILE REFERENCE: 021288-001300US
; CURRENT APPLICATION NUMBER: US/10/237,467
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/317,879
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
; OTHER INFORMATION: 7 (DRG7) (NT009307)
US-10-237-467-9

Query Match 87.3%; Score 845.8; DB 15; Length 909;
Best Local Similarity 99.8%; Pred. No. 3.5e-253;
Matches 847; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 121 GCGGTGACAGAAACGCGGTTGTGCTCTGGCTCTGGGCTGCCCATGCGCAGGAAGCT 180
Db 61 GCGGTGACAGAAACGCGGTTGTGCTCTGGCTCTGGGCTGCCCATGCGCAGGAAGCT 120
QY 181 GTCTCCATCTACATCTCAACCTCTGTGCGCGCGACTTCTCTTCTTAGCGGCACATT 240
Db 121 GTCTCCATCTACATCTCAACCTCTGTGCGCGCGACTTCTCTTCTTAGCGGCACATT 180
QY 241 ATATGTTCCGCTTACGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTCAGTCT 300
Db 181 ATATGTTCCGCTTACGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTCAGTCT 240
QY 301 GTGATGACCTTCTCCCTACTTATAGGCTTAGCATGTGAGCGCCATCAGCAGCCGAGCG 360
Db 241 GTGATGACCTTCTCCCTACTTATAGGCTTAGCATGTGAGCGCCATCAGCAGCCGAGCG 300
QY 361 TGCCTGTCCATCTCTGGCCCATCTGTGACCACTGCGCGCCGCCCCAGATCTCTCATCG 420
Db 301 TGCCTGTCCATCTCTGGCCCATCTGTGACCACTGCGCGCCGCCCCAGATCTCTCATCG 360

QY 421 GTCATGTGTCTGCTCTGGCCCTCTCCCTGCTCGGAGTATCTCTGGAGTGATGTC 480
Db 361 GTCATGTGTCTGCTCTGGCCCTCTCCCTGCTCGGAGTATCTCTGGAGTGATGTC 420
QY 481 TGTGACTTCTCTGTTTGTAGTGTGCTGATCTGTTTGTGTGAACGTCAGATTTCAATACA 540
Db 421 TGTGACTTCTCTGTTTGTAGTGTGCTGATCTGTTTGTGTGAACGTCAGATTTCAATACA 480
QY 541 ATCCGGTGGCTGTTTATGTGTGTTCTCTGTGGTCCAGCCTGCTGCTGCTGCTG 600
Db 481 ATCCGGTGGCTGTTTATGTGTGTTCTCTGTGGTCCAGCCTGCTGCTGCTGCTG 540
QY 601 AGGATTCCTCTGTGGATCCCGGAAGATCCGCTGACCAAGGCTGTACGTGACCAATCTCTC 660
Db 541 AGGATTCCTCTGTGGATCCCGGAAGATCCGCTGACCAAGGCTGTACGTGACCAATCTCTC 600
QY 661 ACAGTGTGCTTCTCTCTCTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 601 ACAGTGTGCTTCTCTCTCTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTCTG 780
Db 661 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTCTG 720
QY 781 TCCGCTCTTAACAGCAGTGGCAACCCCATCATTTACTTCTCTGGGCTCTCTTAGGCAG 840
Db 721 TCCGCTCTTAACAGCAGTGGCAACCCCATCATTTACTTCTCTGGGCTCTCTTAGGCAG 780
QY 841 CGTCAAAATAGGCGAAGACCTGAAGCTGGTCTTCCAGAGGCTCTGCGAGCACGCTGAG 900
Db 781 CGTCAAAATAGGCGAAGACCTGAAGCTGGTCTTCCAGAGGCTCTGCGAGCACGCTGAG 840
QY 901 GTGGATGAAGTGGAGGCTGGCTTCTCAGAAACCTTGGAGCTGTCCGGAAGCAGATTG 960
Db 841 GTGGATGAAGTGGAGGCTGGCTTCTCAGAAACCTTGGAGCTGTCCGGAAGCAGATTG 900
QY 961 GAGCAGTGA 969
Db 901 GAGCAGTGA 909

RESULT 11
US-09-995-225-17
; Sequence 17, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358

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; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-17

Query Match      86.0%; Score 833; DB 9; Length 969;
Best Local Similarity 91.2%; Pred. No. 3.6e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAAGGAGTGGAG 60
DB 1 ATGGATCCAAACCGTCCAGTCTTGGGTACAAAACCTGACACCAATCAAGGAGTGGAG 60
QY 61 ACTCCTTGCTACAAGCAGACCCCTGAGCTTACGGGCTGACGTGCATCGTTTCCCTGTC 120
DB 61 ACTCCTTGCTACAATCAGACCCCTGAGCTTACGGTGCATCGTGCATCATTTCCCTGTC 120
QY 121 GGGTACAGAGAAACCGGTTGTCTGCTCTGGGCTCGGCTCGGATGCGAGAACGCT 180
DB 121 GGAATACAGAGAAACCGGTTGTCTGCTCTGGGCTCGGCTCGGATGCGAGAACGCT 180
QY 181 GTCTCCATCTACATCCTCAACCTGTGCGGGCGGCTTCTCTCTTAGCGGCCACATT 240
DB 181 GTCTCCATCTACATCCTCAACCTGTGCGGGCGGCTTCTCTCTTAGCGGCCACATT 240
QY 241 ATATGTTCCGGTTACGCTCTATCAATATCCGCCATPCCCATCTCAAAATCTCAGTCT 300
DB 241 ATAGTTTCGCCATTAGCCCTCATCAATATCAGCCATCTCATCCGCAAAATCTCAGTCT 300
QY 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCCTAAGCATGCTGAGCGCCATCAGCAGCCGCG 360
DB 301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCCTAAGCATGCTGAGCGCCATCAGCAGCCGCG 360
QY 361 TGCTGTCCATCCTGTGGCCCATCTGGTACCACTGCGCGCGCCCGCCAGATACCTGTCACTG 420
DB 361 TGCTGTCTGTTCTGTGGCCCATCTGGTACCGCTGCGCGCGCCCGCCAGATACCTGTCACTG 420
QY 421 GTCATGTGTCTGCTGTGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTC 480
DB 421 GTCGTGTGTCTGCTGTGGGCGCTGTCCCTGCTGTTTAGTATGCTGGAGTGGAGGTC 480
QY 481 TGTGACTTCTGTTTAGTGGTGTGATTTCTGTTTGGTGTGAACCGTCAGATTTCAATTACA 540
DB 481 TGTGACTTCTGTTTAGTGGTGTGATTTCTAGTTGGTGTGAACCGTCAGATTTCAATCCA 540
QY 541 ATCGGTGGCTGTTTTTTTATGTGTGTTCTCTGTGGGTCCAGCGCTGCTGCTGTGTC 600
DB 541 GTCGGTGGCTGATTTTTTTTATGTGTGTTCTCTGTGTTTCCAGCGCTGCTGCTGTGTC 600
QY 601 AGGATCTCTGTGGATCCCGGAGATGCCGCTGACCAAGCTGTAGTGCACCATCTCTCTC 660
DB 601 AGGATCTCTGTGGATCCCGGAGATGCCGCTGACCAAGCTGTAGTGCACCATCTCTCTC 660
QY 661 ACAGTCTGGTCTTCTCTCTGTGGCCCTGCCCTTTGGCAATTCAGTGGGCCCTGTTTCC 720
DB 661 ACAGTCTGGTCTTCTCTCTGTGGCCCTGCCCTTTGGCAATTCAGTGGGCCCTGTTTAC 720
QY 721 AGGATCCACTGATTTGGAAGTCTTATTTTGTGTCATCTAGTTTCCATTTCTG 780
DB 721 AGGATCCACTGATTTGGAAGTCTTATTTTGTGTCATCTAGTTTCCATTTCTG 780
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QY 781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCATTTACTTCTTCTGGGCTCCTTTAGGCAG 840
DB 781 TCTCTCTTAAACAGTAGTGCACCAACCCCATCATTTACTTCTTCTGGGCTCCTTTAGGCAG 840
QY 841 CGTCAAAATAGGACAGACCTGAAGCTGGTTCTCCAGAGGCTCTGACAGGACACGCTGAG 900
DB 841 CGTCAAAATAGGACAGACCTGAAGCTGGTTCTCCAGAGGCTCTGACAGGACACGCTGAG 900
QY 901 GTGGATCAAGGTGAGGGTGGCTTCCCTCAGAAACCTCGAGCTGTGCGGAAGCAGATTG 960
DB 901 GTGGATAAAGGTGAAGGCGAGCTTCTGAGAAAGCTGAGGCTGTGCGGAAGCAGATTG 960
QY 961 GAGCAGTGA 969
DB 961 GGGCCATGA 969

RESULT 12
US-09-995-225-17
; Sequence 17, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9- Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-17
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Query Match      86.0%; Score 833; DB 10; Length 969;
Best Local Similarity 91.2%; Pred. No. 3.6e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAAGGAGTGGAG 60
DB 1 ATGGATCCAAACCGTCCAGTCTTGGGTACAAAACCTGACACCAATCAAGGAGTGGAG 60
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Db 721 AGGATGACCTGAAATTTGGAAGTCTTATATTTGTCATGTTTATCTGGTTGATGTCCTG 780
Qy 781 TCCGCTCTTAACAGCAGTGCCAAACCCCATCATTTTACTTCTTCGTGGGCTCCTTTAGGCAG 840
Db 781 TCCCTCTTAACAGTAGTGCCAAACCCCATCATTTTACTTCTTCGTGGGCTCCTTTAGGCAG 840
Qy 841 CGTCAAAATAGGCAGAACCTGAAGCTGTTCTCAGAGGGCTCTGCAGGACACGCCCTGAG 900
Db 841 CGTCAAAATAGGCAGAACCTGAAGCTGTTCTCAGAGGGCTCTGCAGGACACGCCCTGAG 900
Qy 901 GTGGATGAAGGTGAGGGGTGCTTCTCAGGAACCCCTGGAGCTGTGGGAAGCAGATTG 960
Db 901 GTGGATGAAGGTGAGGGCAGCTTCTCAGGAACCCCTGGAGCTGTGGGAAGCAGATTG 960
Qy 961 GAGCAGTGA 969
Db 961 GGGCCATGA 969

RESULT 14
US-10-292-798-1041
; Sequence 1041, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1041
; LENGTH: 1369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1369)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1169)
US-10-292-798-1041

Query Match 86.0%; Score 833; DB 16; Length 1369;
Best Local Similarity 91.2%; Pred. No. 4.1e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ATGGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60
Db 201 ATGGATCAACCATCCAGCTTCCGTATCAAAAACCTGACCAATCAACGGACGTGAGGAG 260
Qy 61 ACTCCTTGCTACAAGCAGACCCCTGAGCTTCACGGGGCTGACGTGATCGTTTCCCTTGTG 120
Db 261 ATCTCTTGCTACAATCAGACCCCTGAGCTTCACGGGTGCTGACGTGATCATTTCCCTTGTG 320
Qy 121 GCGCTGACAGGAAACCGCGTTGTGCTTGGCTTCCTGGGTGCGGTGCGGTGCGGTGCGGTGCGGT 180
Db 321 GGAAGTACAGGAAACCGCGTTGTGCTTGGCTTCCTGGGTGCGGTGCGGTGCGGTGCGGTGCGGT 380
Qy 181 GTCCTCATCTACATCTCAACTGGTTCGGGGCGGACTTCTCTTCTTCTTAGCGGCGCACATT 240
Db 381 GTCCTCATCTACATCTCAACTGGTTCGGGGCGGACTTCTCTTCTTCTTAGCGGTTCAGATT 440
Qy 241 ATATGTTCCCGCTTACGCGCTCAATATATCGCCCATCCATCTCCAAATCTCTCAGTCTCT 300
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Db 441 ATACGTTTCCCATAGCCTCATCAATATAGCCATCTCATCCGAAATCTCGTTTCT 500
Qy 301 GTGATGACCTTCCCTACTTTATAGGCCCTTAAGCATGCTGAGGCCCATCAGCACCGAGCGC 360
Db 501 GTGATGACCTTCCCTACTTTATAGGCCCTTAAGCATGCTGAGGCCCATCAGCACCGAGCGC 560
Qy 361 TGCCTGTCCATCCTGTGGGCCCATCTGGTACACTGCGCGCGCGCCGACAGTACCTGTCATCG 420
Db 561 TGCCTGTCTGTTCTGTGGGCCCATCTGGTACACTGCGCGCGCGCCGACACACCTGTGAGCG 620
Qy 421 GTCATGTGTCTCTGTCTGGGCCCTGTCTCTGCTGCGGAGTATCTCTGAGTGGAGTGTTC 480
Db 621 GTCGTGTGTCTCTGTCTGGGCCCTGTCTCTGCTGCTGTTTAGTATGCTGAGTGGAGTGTTC 680
Qy 481 TGTGACTTCTCTGTGTAGTGGTCTGATTTCTGTTTGGTGTGTAAGTGTGAAACGTGAGATTTCATTACA 540
Db 681 TGTGACTTCTCTGTGTAGTGGTCTGATTTCTGTTTGGTGTGTAAGTGTGAAACGTGAGATTTCATTACA 740
Qy 541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTTCCTGTGGGTCCAGCTGGTCTGCTGTGTC 600
Db 741 GTCCGCTGGCTGATTTTTTTTATGTGTGGTTCCTGTGTGTTCCAGCCTGGTCTGCTGTGTC 800
Qy 601 AGGATTCCTGTGGATCCCGGAAGATGCCGCTGACAGGCTGTACGTGACCATCTCTCTCTC 660
Db 801 AGGATTCCTGTGGATCCCGGAAGATGCCGCTGACAGGCTGTACGTGACCATCTCTCTCTC 860
Qy 661 ACAGTGTCTGCTCTCTCTCTCTCTGTGGCTGCGCTTGGCAATTCAGTGGGCCCTGTTTTCG 720
Db 861 ACAGTGTCTGCTCTCTCTCTCTCTGTGGCTGCGCTTGGCAATTCAGTGGGCCCTGTTTTCG 920
Qy 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTATGTGTCATGTGTCATTTTCCATTTTCCCTG 780
Db 921 AGGATGACCTGAAATTTGGAAGTCTTATATTTGTATGTGTCATTTTATCTGTTTTCATGTCCCTG 980
Qy 781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCATTTTCTCTGCTGGGCTCTCTTTAGGCAG 840
Db 981 TCCTCTCTAAACAGTAGTGCACCAACCCCATCATTTTCTCTGTTGGGCTCTCTTTAGGCAG 1040
Qy 841 CGTCAAAATAGGCAGAACCTGAAAGTGTCTTCCAGAGGGCTCTGCAGGACAGCCTGAG 900
Db 1041 CGTCAAAATAGGCAGAACCTGAAAGTGTCTTCCAGAGGGCTCTGCAGGACAGCCTGAG 1100
Qy 901 GTGGATGAAGGTGAGGGTGGCTTCTCTCAGGAACCCCTGAGGCTGTCGGGAGCAGATTG 960
Db 1101 GTGGATGAAGGTGAGGGCAGCTTCTTGAGGAAGCCTGGAGCTGTCGGGAAGCAGATTG 1160
Qy 961 GAGCAGTGA 969
Db 1161 GGGCCATGA 1169

RESULT 15
US-10-183-116-32
; Sequence 32, Application US/10-83116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE 4C1CP1
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
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; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (433)...(1398)
US-10-183-116-32

Query Match      86.0%; Score 833; DB 15; Length 1604;
Best Local Similarity 91.2%; Pred. No. 4,4e-249; Mismatches 85; Indels 0; Gaps 0;
Matches 884; Conservative 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCGTGAGGAG 60
Db 433 ATGGATCCCAACCGTCCCACTTCGGGTACAAACTGACACCAATCAACGGAGCGTGAGGAG 492

QY 61 ACTCCTTGCTACAGAGACCGCTGAGCTTCAGGGGCTGACGTGCATCGTTCCCTTGTG 120
Db 493 ACTCCTTGCTACAAATCAGACCGCTGAGCTTCAGGGTCTGACGTGCATCATTTCCCTTGTG 552

QY 121 GCGCTGACAGGAAACCGGTTGTCTCTGGCTCTGGGCTGCCGATGCCAGGAACGCT 180
Db 553 GGACGTGACAGGAAACCGGTTGTCTCTGGCTCTGGGCTGCCGATGCCAGGAACGCT 612

QY 181 GTCTCCATCTACATCTCAACCTGTGGCGGGCGAGCTTCTCTTCTTAGCGGCCACATT 240
Db 613 GTCTCCATCTACATCTCAACCTGTGGCGGGCGAGAGCTTCTCTTCTTAGCGTTCCAGATT 672

QY 241 ATATGTTCCGCGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
Db 673 ATAGTTCCGCGTTAGCGCTCATCAATATCCGCCATCTCATCCGCAAAATCTCTGTTCT 732

QY 301 GTGATGACCTTTCCCTACTTTATAGCCCTAAGCATCTGAGCGCCATCAGCACCGAGCGC 360
Db 733 GTGATGACCTTTCCCTACTTTATAGCCCTGAGTATCTGAGCGCCATCAGCACCGAGCGC 792

QY 361 TGCTGTCCATCTGTGGCCATCTGTGTACCACTGCGCGCCGCCAGATACCTGTCACTCG 420
Db 793 TGCTGTCTGTTCTGTGGCCATCTGTGTACCGCTGCGCGGCCCCACACACCTGTCACTCG 852

QY 421 GTCATGHTGTCCTGTCTGGGCCCTGTCCCTGCTCGGAGATACCTGAGTGGATGTTTC 480
Db 853 GTGCTGTGTCCTGTCTGGGCCCTGTCCCTGCTCTTTAGTATGCTGGAGTGGAGGTTTC 912

QY 481 TGTGACTTCTGTTAGTGGTGTGATTTCTGTTTGGTGTGAACGTCAGATTTTATTACA 540
Db 913 TGTGACTTCTGTTAGTGGTGTGATTTCTGTTTGGTGTGAACGTCAGATTTTATTACA 972

QY 541 ATCCGCTGGCTGTTTTTTTATGTGGTCTCTGTGGGTCAGGCTGTCTGTCTGTCTG 600
Db 973 GTCCGCTGGCTGTTTTTTTATGTGGTCTCTGTGGTCTCCAGCTGTCTGTCTGTCTG 1032

QY 601 AGGATCTCTGTGGATCCCGAGAGTCCGCTGACAGGCTGTACGTGACCATCTCTCTC 660
Db 1033 AGGATCTCTGTGGATCCCGAGAGTCCGCTGACAGGCTGTACGTGACCATCTCTCTC 1092

QY 661 ACAGTGTGCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 1093 ACAGTGTGCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152

QY 721 AGGATCCACTGATTTGGAAGTCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1153 AGGATCCACTGATTTGGAAGTCTTATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1212

QY 781 TCCGCTCTTAACAGACAGTGCACCCCATCATTTACTTCTTCTGCTGGGCTCTTTAGGCAG 840
Db 1213 TCCTCTCTAACAGACAGTGCACCCCATCATTTACTTCTTCTGCTGGGCTCTTTAGGCAG 1272
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QY 841 CGTCAAAATAGCGAGAACCTGAAGCTGTTCTCCAGAGGGCTCTCCAGGACACGCTTGAG 900
Db 1273 CGTCAAAATAGCGAGAACCTGAAGCTGTTCTCCAGAGGGCTCTCCAGGACACGCTTGAG 1332

QY 901 GTGGATGAAGGTGGAGGGTGGCTTCTCTCAGGAAACCTCTGAGAGCTGTCTGGGAAAGCAGATTG 960
Db 1333 GTGGATGAAGGTGAAGGGCAGCTTCTCTGAGGAAAGCTCTGAGAGCTGTCTGGGAAAGCAGATTG 1392

QY 961 GAGCAGTGA 969
Db 1393 GGGCCATGA 1401
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Search completed: July 4, 2004, 08:42:22
Job time : 528 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 05:06:47 ; Search time 3093 Seconds
(without alignments)
9355.465 Million cell updates/sec

Title: US-09-787-879C-3

Perfect score: 969

Sequence: 1 attgattcaaccatccagc.....gaagcagattggagcagtgga 969

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931050276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_esti:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682.2	70.4	889	14	CA455045
2	604.4	62.4	764	12	BG198766
3	559.8	57.8	688	10	BE439409
4	548.2	56.6	757	12	BG208126

C	5	486.4	50.2	871	12	BG210740
	6	457.2	47.2	924	14	CD051096
	7	358.8	37.0	503	28	AQ888076
	8	347	35.8	468	28	B74348
	9	343	35.4	2075	11	AK029369
	10	335.4	34.6	620	28	AQ696198
	11	297.4	30.7	905	14	CD243595
	12	285.6	29.5	618	12	B1828553
	13	284.6	29.4	704	13	B741352
	14	279.8	28.9	783	14	CD469424
C	15	279.2	28.8	515	9	AL705589
	16	276.4	28.5	765	14	CD469412
	17	274	28.3	770	14	CD469131
	18	273.8	28.3	777	14	CD467625
	19	273.2	28.2	576	14	CD469125
	20	272.6	28.1	725	14	CD468987
	21	272.6	28.1	761	14	CD467287
	22	270.8	27.9	719	14	CD469292
	23	270.2	27.9	503	9	AF003828
	24	264.8	27.3	756	14	CD469433
C	25	262	27.0	682	28	AZ346449
	26	242.2	25.0	639	14	CD467510
	27	241.2	24.9	634	14	CD471204
	28	241.2	24.9	634	14	CD471217
	29	241.2	24.3	644	14	CD469330
	30	239.6	24.7	637	14	CD467799
	31	237.6	24.5	644	14	CD470186
	32	235.4	24.3	630	14	CD470076
	33	230	23.7	767	14	CD467920
	34	229.2	23.7	634	14	CD535184
	35	229	23.6	618	14	CD470897
	36	228.4	23.6	664	14	CD535223
	37	228.4	23.6	669	14	CD535616
	38	228	23.5	621	14	CD470214
	39	227.6	23.5	704	13	BY741329
	40	227	23.4	515	28	AZ602580
	41	222	22.9	733	13	BY741303
	42	219.4	22.6	484	10	BB853701
	43	217	22.4	633	14	CD470991
	44	215.6	22.2	603	14	CD469303
	45	210.8	21.8	627	14	CD471307

ALIGNMENTS

RESULT 1
CA455045
LOCUS CA455045
DEFINITION AGENCOURT_10735784 MAPcL Homo sapiens cDNA clone IMAGE:6722551 5',
mRNA sequence.
ACCESSION CA455045
VERSION CA455045.1 GI:24905369
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Library of Medicine
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: sgabbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (ILLN)
Cloning by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1485 row: h column: 07
High quality sequence stop: 743.

FEATURES		Location/Qualifiers	
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		/clone="IMAGE:6722551"	
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		/lab_host="EMD108"	
		/clone_lib="WAPcL"	
		/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."	
ORIGIN		70.4%; Score 682.2; DB 14; Length 889; Query Match Best Local Similarity 97.8%; Pred. No. 1.2e-149; Matches 701; Conservative 0; Mismatches 15; Indels 1; Gaps 1;	
QY	1	ATGATTCAACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG	60
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QY	61	ACTCCTTGCTACAGCAGACCCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTG	120
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QY	121	GGCGTACAGAAACGGGTGTGCTCTGGCTCTGCGGTGCGGATGCGGAGACGCT	180
Db	293	GGCGTACAGAAACGGGTGTGCTCTGGCTCTGCGGTGCGGATGCGGAGACGCT	352
QY	181	GTCTCCATCATCTCCATCACTGGTGGCGGCGACTTCCTCTTCTTACGCGCCACATT	240
Db	353	GTCTCCATCTGCATCTCAACTGGTGGCGGCGACTTCCTCTTCTTACGCGCCACATT	412
QY	241	ATATGTTGGCGTTACGCTCATCAATATCGGCATCCCATCTCCAAATTCCTCATCTCT	300
Db	413	ATATGTTGGCGTTACGCTCATCAATATCGGCATCCCATCTCCAAATTCCTCATCTCT	472
QY	301	GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGTGAGCGCCATCAACCGGAGCG	360
Db	473	GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGTGAGCGCCATCAACCGGAGCG	532
QY	361	TGCGTGCATCTGTGGCCCATCTGTACACATCGCGCGCCGCCAGATACCTGTCAACG	420
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QY	421	GTCAATGTGTCCTGTGGCCCTGTCCCTGTGCGGAGTATCTCTGGAGTGGATGTTT	480
Db	593	GTCAATGTGTCCTGTGGCCCTGTCCCTGTGCGGAGTATCTCTGGAGTGGATGTTT	652
QY	481	TGTGACCTTCCCTGTAGTGTGCTGATCTGTTGGTGTGAACGTCAGATTTCAATACA	540
Db	653	TGTGACCTTCCCTGTAGTGTGCTGATCTGTTGGTGTGAACGTCAGATTTCAATACA	712
QY	541	ATCCGTGGCTGCTTTTATGTTGTTCTGTGCTGCGGATATCTCTGGAGTGGATGTTT	600
Db	713	ATCCGTGGCTGCTTTTATGTTGTTCTGTGCTGCGGATATCTCTGGAGTGGATGTTT	772
QY	601	AGGATTCCTGTGGATCCCGAAGATGCGGTGACACGAGCTGTACGTGACCATCTCTCTC	660
Db	773	AGGATTCCTGTGGATCCCGAAGATGCGGTGACACGAGCTGTACGTGACCATCTCTCTC	832
QY	661	ACAGTGTGCTTCC-TCCCTGTGGCTGCTCCCTTTGGCATTCAGTGGGCCCTGTT	716
Db	833	ACAGTGTGCTTCCCTCTGTGGCTGCTCCCTTTGGCATTCAGTGGGCCCTT	889

RESULT 2		764 bp mRNA linear EST 21-APR-2003	
BG198766		R518035 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.	
EST		GI:13720453	
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 764)			
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Petry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Bozzer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.			
Creation of genome-wide protein expression libraries using random activation of gene expression			
Nat. Biotechnol. 19 (5), 440-445 (2001)			
21227151			
11329013			
Contact: Scott J. Cain			
Athersys, Inc.			
3201 Carnegie Ave, Cleveland, OH 44115, USA			
Tel: 216 431 9900			
Fax: 216 361 9596			
Email: scain@atersys.com			
High quality sequence stop: 559.			
Location/Qualifiers			
1..764			
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/cell_line="HT1080"			
/clone_lib="Athersys RAGE Library"			
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."			
ORIGIN		62.4%; Score 604.4; DB 12; Length 764; Query Match Best Local Similarity 89.6%; Pred. No. 2.3e-131; Matches 672; Conservative 0; Mismatches 76; Indels 2; Gaps 2;	
QY	187	ATCTACATCCTCAACCTGTGTGCGGCGCGACTTCCTCTTCTTATAGC-GGCCACATTATATG	245
Db	764	ATCTACATCCTCAACATGGCGCGCAGACAGATTCCTGTCTCAGCGCGCGCTTATATA	705
QY	246	TTGCGCGTTACGCTCATCAATAT-CCGCGATCCCATCTCCAAATCCTCAGTCTCTGTA	304
Db	704	TTCCCTGTTAGCTTTTCATCAGTATCCCGCCATCATCTCTTAAATCCTCTATCCTGTGA	645
QY	305	TGACCTTTTCCCTACTTTATAGGCTTAAGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCC	364
Db	644	TGATGTTTCTTACTTTTTCAGGCGCTGAGCTTCTTGAGTGGCGTGGAGCGAGCGCTGCC	585
QY	365	TGTCCATCTGTGGGCCCATCTGTGTACCACTGCGCGCGCCCGACAGATCTGTCTCATCGTCA	424
Db	584	TGTCCGCTCTGTGGGCCCATCTGTGTACCGCTGTCACACCGCCCGCACACCTGTFCAGCGGTGG	525
QY	425	TGTGTCTGCTGTCTGGGCCCTGTCCCTGTCTGCGAGTATCCTCGAGTGGATGTTCTGTG	484
Db	524	TGTGTGTCTGTCTGTGGGCCCTGTCCCTGTCTGCGAGAGCATCTCTGGAGTGGATGTTATGTG	465
QY	485	ACTTCTCTGTTTGTGTGTCTGATTCTGTGTTGGTGTGAAAAGCTCAGATTTTCATTCAATTCG	544
Db	464	GC-TTCTGTTCAGTGGTGTGTGATTCTGTGTTGGTGTCAAAATCATCAGATTTTCATCAGTCG	405
QY	545	CGTGGCTGTTTTTTTTTATGTGTGTTCTCTGTGGGCTCAGCGCTGTCTCTGTGTCTGTCAGGA	604

RESULT 2																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Db      404 CGTGCCTGATTTTTTATGTTGTTCTCTGTGGTCCAGCCGCTCTGCTGATCAGGA 345
QY      605 TTCTCTGTGGATCCGGAGATGCCGCTGACGAGCTGTAGTGACCACTCTCTCTACAG 664
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Db      284 TACTGGTCTTCTCTCTGTGGCTGCCCTTTGGCAATTCAGTGGGCCCTGTTTTCCAGGA 225
QY      725 TCCACTGGATGGAAAGTCTTATTTGTGATGTCATCTAGTTTCCATTTCTCTGTCCG 784
Db      224 TCCAGTGGACAGGGAAGTCTTATTTGTGATGTTTCTATGTTTCTATTTCTCTGTCCG 165
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Db      164 CTCTTAAACAGCAGTGCACACCCCATCTTACTTCTGCTGGCTCCCTTTAGGAGCGTC 105
QY      845 AAAATAGGAGAACCTGAACTGTTCTCCAGAGGCTCTGACGACACGCTGAGGTGG 904
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Db      44 ATGAGGTGGAGGCGAGAAATCTGAGGAAA 15

RESULT 3
BE439409
LOCUS   HTM1-025F1 HTM1 Homo sapiens cDNA, mRNA linear EST 25-JUL-2000
DEFINITION
ACCESSION BE439409
VERSION   BE439409.1 GI:9438891
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL  1 (bases 1 to 688)
COMMENT  Gonzalez, P., Epstein, D.L. and Borras, T.
        Characterization of gene expression in human trabecular meshwork
        using single-pass sequencing of 1060 clones
        Invest. Ophthalmol. Vis. Sci. (2000) In press
        Contact: Pedro Gonzalez
        Department of Ophthalmology
        Duke University
        Duke Eye Center, Erwin Rd, Box 3802, Durham, NC 27710-3802, USA
        Tel: 919 681 4085
        Fax: 919 684 8983
        Email: pedro.gonzalez@duke.edu
FEATURES
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ORIGIN
Query Match 57.8%; Score 559.8; DB 10; Length 688;
Best Local Similarity 98.7%; Pred. NO. 6.9e-121;
Matches 627; Conservative 0; Mismatches 2; Indels 6; Gaps 6;

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QY      61 ACTCTTGTGTACAGAGACCTTACGCTTCAACGGGCTGACGTGCAATCTCTTCCCTTGTTC 120
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QY      121 GCGCTGACAGGAAACGGGGTGTGCTCTGGCTCTCTGGCTGCGCATGCGCAGGAACGCT 180

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Db      180 GCGCTGACAGGAAACGGGGTGTGCTCTGGCTCTCTGGCTGCGCATGCGCAGGAACGCT 239
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Db      240 GTCTTCATCTACATCTCAACCTGTCGCGGCGGACTTCTCTTCTTACGCGCCACATT 299
QY      241 ATATGTTGCGCGTTACGCTCATCAATATCCGCAATCCCATCTCCAAAATCTCTCAGTCT 300
Db      300 ATATGTTGCGCGTTACGCTCATCAATATCCGCAATCCCATCTCCAAAATCTCTCAGTCT 359
QY      301 GTATGACCTTTCCCTACTTATAGCGCTTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 360
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QY      361 TGCTGTGCATCTGTGGCCCATCTGTACTACCACTGCGCGCCGCCAGATACCTGTCTATCG 420
Db      420 TGCTGTGCATCTGTGGCCCATCTGTACTACCACTGCGCGCCGCCAGATACCTGTCTATCG 479
QY      421 GTATGTGTGTCTGTCTGGGCCCTGCTCCCTGCTCGGAGTATCTCGAGTGGATGTTTC 480
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QY      481 TGTGACTTCTCTGTTAGTGTCTGATTCTGTTTGTGTGAACAGTCAAGATTTTCATTACA 540
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QY      541 ATCGCGTGGCTGTTTTTATGTGTGTCTCTGTGGTCCAGCTGTCTCTGCTGCTGCTC 600
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QY      601 AGGATTCCTGTGATCCCGGAAGATGCCGCTGAC 635
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RESULT 4
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LOCUS   BG208126 787 bp mRNA linear EST 21-APR-2001
DEFINITION
ACCESSION RST27616 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
VERSION   BG208126
KEYWORDS BG208126.1 GI:13729813
SOURCE   EST.
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL  1 (bases 1 to 787)
COMMENT  Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
        Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,
        Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
        Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
        Offenbacher, J., Danzig, J. and Ducar, M.
        Creation of genome-wide protein expression libraries using random
        activation of gene expression
        Nat. Biotechnol. 19 (5), 440-445 (2001)
        21227151
        PUBMED 11329013
        COMMENT Contact: Scott J. Cain
        Athersys, Inc.
        3201 Carnegie Ave, Cleveland, OH 44115, USA
        Tel: 216 431 9900
        Fax: 216 361 9596
        Email: scain@athersys.com
        High quality sequence stop: 553.
        Location/Qualifiers
        1..787
         /organism="Homo sapiens"
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         /db_xref="taxon:9606"
         /cell_line="HT1080"
         /clone_lib="Athersys RAGE Library"
         /note="See 'Creation of Genome-wide Protein Expression

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Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 56.6%; Score 548.2; DB 12; Length 787;
Best Local Similarity 86.9%; Pred. No. 3.9e-118;
Matches 649; Conservative 0; Mismatches 93; Indels 4;
Gaps 5;

QY 196 CTCACCTGTGCGCGCGACTCTCTCTTCTAGCGGCCACATATATGTTCCGCGTTA 255
DB 747 CTGAGCTGGGGGGGGGACTTCTCTTCTTACAGCCACAGAT-CCATCCCTGTTA 589

QY 256 CGGCTCATCAATATCCGCCATCCCATCTCAAAATCTCAGTCTCTGTGATGACTTCC 315
DB 688 CGGCTCATCAATAGCTCCATCCATCTCTAATCTCTTAGCTGTGATGACTTCC 629

QY 316 TACTTTATAGGCTTAAGCTGCTGAGCGCCATCAGCACGAGCGCTGCTGCCATCC 375
DB 628 TACTTGGCAGGCTGAATATCTGAGTGCCATGAGCACCAAGCGCTGCTCAATCC 569

QY 376 TGGCCCATCTGTTACCACTCGCGCGCCGCCAGATACCTGTCTCATCTGTGTCCT 435
DB 568 TGGCCCATCTGTTAAAGCTCGCGCCACCC-ACACCTGCCAACGGTGTGTGTCCT 511

QY 436 CTCGCGCCCTGCTCCGCTGCGGAGTATCTCGAGTGGATGTTCTGTGACTTCC 495
DB 510 CTCGCGCCCTGCTCCGCTGAGAGCATCTGAGTGGATGTTCTGTGACTCCCT 451

QY 496 AGTGGTCTGATCTGTTTGGTGTGAACGTCTAGATTTCAATCAATCGCGTGGCT 555
DB 450 AGTGATCTGATCTGTTTGGTGTCAAAATCAGA-TTCATCAGTTACGTGGCTGAT 392

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DB 391 TTTTATTTGTGTGCTCTGTGTGCCAGCTGTCTGTAGTGTCTGAGTATCTCTGGA 332

QY 616 TCCCGGAAGATCGCGCTGACGAGCTGTAGTGACCATCTCTCTCAGTGTGGCTTC 675
DB 331 TCCAGAGATGCCACTGACGAGCTGTACATGACCAT-CTGTCTCAGTGTGGCTTC 273

QY 676 CTCCTCTGTGCGCTTGTGGCATTCAGTGGGCTGTGTTTCCAGGATCCACCTGGAT 735
DB 272 CTCCTCTGTGCGCTTGTGGCATTCAGTGGGCTGTGTTTCCAGGATCCACATGGAC 213

QY 736 TGGAAAGTCTTATTTGTCTATGTCATCTAGTTTCCATTTCTGTCTCCGCTCTTAACAGC 795
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QY 796 AGTCCCAACCCCATCATTTACTTCTCTGGGCTCTTTAGGAGCGCTCAAAATAGGAG 855
DB 152 AGTCCCAACCCCATCATTTACTTCTCATGGGTTCTGTAGGAGCATCAAAATAGGAG 93

QY 856 AACCTGAGCTGTTCTCCAGAGGCTCTGAGGAGCGCTGAGGTTGATGAAGTTGA 915
DB 92 AACCTGAGCTGTTCTCCAGAGGATCTGAGGAGCGCTGAGGTTGATGAAGTTGA 33

QY 916 GSGTGGTCTTCTCAGGAACCCCTGGAG 942
DB 32 TGGTGGTATCTCAGGAACCCCTGGAG 6

RESULT 5
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LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM

871 bp
mRNA
linear
EST 21-APR-2001
RST30287
BG210740
BG210740.1
GI:13732427
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 871)

REFERENCE
AUTHORS

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,
Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE
JOURNALMEDLINE
PUBMED

COMMENT

Contact: Scott J. Cain

Athersys, Inc. Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 456.

Location/Qualifiers

source

1..871

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="HT1080"

/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 50.2%; Score 486.4; DB 12; Length 871;
Best Local Similarity 90.9%; Pred. No. 1.5e-103;
Matches 528; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

QY 354 CGAGCGCTGCGCTTCCATCTCTGTGCGCCATCTGTGTACACGTCCCGCGCCGACATACCT 413
DB 580 CGAACCCCGCTGTCCGCTCTGT-GCCCATCTGTGTCCTAGTACCGCCGCCACACCT 522

QY 414 GTCATCGGTGATGTGTCTCTGCGCCCTCTGCTGCGGAGTATCTCTGGAGTG 473
DB 521 GTCAGCGTGTGTGTGTCTTGTCTGCGCCCTGTCTGCTGCGGAGTATCTCTGGAGTG 462

QY 474 GATGTCTGTGACTTCTCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 533
DB 461 GATGT 402

QY 534 GATTAACATCGCGT 593
DB 401 CATCACAGT 342

QY 594 GCTGTGTGAGGATCTCTCTGT 653
DB 341 GCTGTGTGAGGATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 282

QY 654 CTTCTCTCAGT 713
DB 281 CTTCTCTCAGT 222

QY 714 GTTTTCCAGGATCCACCTGGATTTGAAAGTCTTATTTGTGTGTGTGTGTGTGTGTGTGT 773
DB 221 ATTTTATGATTCACGT 162

QY 774 TTTCTGTGCGCTTCTTAACAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 833
DB 161 TTTCTGTGCGCTTCTTAACAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 102

QY 834 TAGGAGCGT 893

Db 52 AAGCTTCATCAGTATCCCCATACCATCTCTAAATCCTCTATCTATCTGCGATGATTTTC 111
 Qy 315 CTACTTTATAGGCTAAGCATGCTGAGCCATCAGCAGCGAGCGCTGCTGCTCCATCCT 374
 Db 112 CTACTTTGAGGCTGAGCTTCTGAGTGGCGTGAGCAGCGAGCGCTGCTGCTGCT 171
 Qy 375 GTGGCCATCTGTTACATGCGGCGCGCCAGATACCTGTATCGGTATGTTGCTT 434
 Db 172 GTGGCCATCTGTTACATGCGGCGCGCCAGATACCTGTATCGGTATGTTGCTT 231
 Qy 435 GCTCTGGGCGCTGCTGCGGAGTATCTGAGTGGATGTTCTGTGACTTCCCTGTT 494
 Db 232 GCTCTGGGCGCTGCTGCGGAGTATCTGAGTGGATGTTCTGTGACTTCCCTGTT 291
 Qy 495 TAGTGTGCTGATCTGTTTGGTGTGAACGTCAGATTTCAATCAATCGCGTGGCTGGT 554
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 Qy 675 CTCTCTGTTGGCTGCGCTTGGCATTTCA 704
 Db 472 CTCTCTGTTGGCTGCGCTTGGCATTTCA 501

RESULT 8

B74348
 LOCUS CIT-HSP-2042L7.TF CIT-HSP Homo sapiens genomic clone 2042L7,
 genomic survey sequence.

ACCESSION B74348.1 GI:2770035

VERSION GSS.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 468)

AUTHORS Adams,M.D., Rounsley S.D., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M. and Venter,J.C.

TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map

JOURNAL Building

COMMENT Unpublished (1997)

Other GSSs: CIT-HSP-2042L7.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

TEL: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: M13-21

Class: BAC ends.

Location/Qualifiers

1. 468

/organism="Homo sapiens"

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FEATURES

source

ORIGIN
 Query Match 35.8%; Score 347; DB 28; Length 468;
 Best Local Similarity 90.3%; Pred. No. 7.3e-71;
 Matches 371; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 Qy 255 AGCGCTCATCAATATCCGCCATCCCATCTCCAAATCCTCAGTCTGTGATGACCTTTCC 314
 Db 57 AAGCTTCATCAGTATCCCCATACCATCTCTAAATCCTCTATCTGTGATGATGTTTC 116
 Qy 315 CTACTTTATAGGCTAAGCATGCTGAGCCATCAGCAGCGAGCGCTGCTGCTCCATCCT 374
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 Db 172 GTGGCCATCTGTTACATGCGGCGCGCCAGATACCTGTATCGGTATGTTGCTT 236
 Qy 435 GCTCTGGGCGCTGCTGCGGAGTATCTGAGTGGATGTTCTGTGACTTCCCTGTT 494
 Db 232 GCTCTGGGCGCTGCTGCGGAGTATCTGAGTGGATGTTCTGTGACTTCCCTGTT 296
 Qy 495 TAGTGTGCTGATCTGTTTGGTGTGAACGTCAGATTTCAATCAATCGCGTGGCTGGT 554
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 Qy 555 TTTTATATGTTGTTCTGTTGGTGTCAACATCATCATTTCAATCAAGACGCGTGGT 614
 Db 352 TTTTATATGTTGTTCTGTTGGTGTCAACATCATCATTTCAATCAAGACGCGTGGT 416
 Qy 615 ATCCGGAATGCGCTGACAGGCTGTACGTGACCATCTCTCAAGTGTGCTT 665
 Db 412 ATCCGGAATGCGCTGACAGGCTGTACGTGACCATCTCTCAAGTGTGCTT 467

RESULT 9

AK029369

LOCUS

DEFINITION

Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched

library, Clone:483406120 product:MrpB2 G protein-coupled receptor,

full insert sequence.

ACCESSION AK029369.1 GI:26325335

VERSION AK029369

KEYWORDS HTC; CAP trapper

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349536

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,

Fujiwaka,S., Inoue,K., Togawa,Y., Ohara,E., Watahiki,M.,

Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,

Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format

/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
 HindIII"

sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2075)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-res@gscl.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]

CNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="MGI:2351462"
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ORIGIN

Query Match 35.4%; Score 343; DB 11; Length 2075;
Best Local Similarity 62.3%; Pred. No. 1.3e-69;
Matches 579; Conservative 0; Mismatches 335; Indels 15; Gaps 2;

QY 28 ACAGAACTGACACCAATCAACGGACGTGAGAGACTCTCTGCTACCAAGACCTGAGC 87
DB 125 ACAGTGTCTGAATGGAAGCTACTACTTCGATACTTTCAGTTTGTGTCCACGAGAACCAAGCC 184
QY 88 TTCACGGGCTGACCTGCTGATGTTTCCCTTGTGCGGCTGACAGGAAACCGGTTGTGCTC 147
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QY 148 TGGCTCTGGGCTGCGGATGCGGATGCGGAGAACGCTGTCTCAATCATCTCAACCTGCTC 207
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QY 268 ATCCGCCATCC-----CATCTCAAAATCCTCAGTCCTGTGATGACCTTCCC 315
DB 365 ATCTTCTACTCAATTGACATCAACATCCCTTTGTTCTTATGTTGTGCCAATATTGCT 424
QY 316 TACTTTATAGGCTAAGCATGCTGAGCGCATCAGCAGCGGCTGCTGTCCATCTG 375
DB 425 TATCTTTCAGGCTCTGAGCATCTCAGACCATTTAGCATGAGCGCTGTGTTCTGTAATA 484
QY 376 TGGCCCATCTGTTACACCTTGGCGCGCCCGCCAGATACCTGTCTATCGGTCTATGTTGCTCTG 435
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DB 665 GTTTTTTTTGGTGTCTCTGTTGGGCTAGCGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
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DB 725 TCACAGCGAATTCCTATGACAGGCTGATGTGACTATTACACTCAGTCTTGTGCTCTTC 784
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QY 736 TGGAAAGTCTTATTTGTCATGTCATCTAGTTTCCATTTTCTGCTCCGCTCTTAAACAGC 795
DB 845 TATTATGTTGAATTTGTAATTTTATCTTGAGATACTATTCCTATCTCTGTTTAAACAGC 904
QY 796 AGTGCCACACCCCATCATTTACTTCTTCTGTTGGGCTCTCTTATAGGACCGCTCAAAATAGCC-- 853
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DB 965 AGAGCTCTCAAGCTACTTCTGAGAGAGCCATGCAAGACACCCCTGAGAGGACAAAGT 1024
QY 913 GGAGGGTGGCTTCTCCAGGAAACCCCTGGA 941
DB 1025 GGAAATAAGAGTCTTTCAGAACACCCCTGA 1053

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RESULT 10
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LOCUS
DEFINITION
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ACCESSION
AQ696198
VERSION
AQ696198.1 GI:5386446
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 620)
  Mahairas.G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  10449764
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones may be purchased from Research Genetics (info@resgen.com).
  BAC end Web Server: http://www.htsc.washington.edu
  Plate: 2142 row: L column: 7
  Seq primer: T7
  Class: BAC ends
  High quality sequence stop: 620.
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  QY 315 CTATTTATAGGCTAAGCATGTGAGCGGCATCAGCACCGAGCGCTGCTGTCCATCCT 374
  DB 112 CTACTCTGCAAGCTGAGCTGATCTGAGTGCCTGAGCAGCAGCGCTGCTGCTGCT 171
  QY 375 GTGCGCATCTGTGTACCACTGCGCGCCCGCATACCTGTCATCGGTGATGTCCT 434
  DB 172 GTGCGCATCTGTGTACCGCTGCGCACCGCCCGCCACACCTGTGAGCGGTGGTGTGTCCT 231
  QY 435 GCTTGTGGCCCTTTCCTGTCGCGAGTATCTCTGGAGTGGATGTTCTGTGACTTCCCTTT 494
  DB 232 GCTGTGGCCCTTTCCTGTCGCGAGTATCTCTGGAGTGGATGTTATGTGCTTCTCTGTT 291
  QY 495 TAGTGGTGTGCTGATTTCTTTGGTGTGAACGTCAGATTTTCATTACATCGGTGCTGTGT 554
  DB 292 CAGTGGTGTGCTGATTTCTGCTTTGGTGTCAACATCATATTTCATCAAGTCTGGTGTCT 350
  QY 555 TTTTATATGTGTGCTTCTGCTGTGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614

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Db 351 TTTTATATGTGTGCTTCTCTGTGGTTCAGCCTGCTGCTGATCAGGATTTCTGTGG 410
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QY 675 CTTCTCTGTGGCTGCTGCTTGG 697
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CD243595      905 bp      mRNA      linear      EST 22-MAY-2003
LOCUS
DEFINITION
  AGENCOURT_14121139 NIH_MGC_180 Homo sapiens cDNA clone
  IMAGE:30393708 5', mRNA sequence.
CD243595
ACCESSION
CD243595
VERSION
CD243595.1 GI:31004059
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 905)
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  cDNA Library Preparation: Invitrogen Corp
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: NDAM447 row: P column: 21
  High quality sequence start: 20
  High quality sequence stop: 592.
  Location/Qualifiers
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      /mol_type="mRNA"
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      /clone="IMAGE:30393708"
      /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
      /note="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NotI;
      Site 2: EcoRV (destroyed); Library is oligo-dT primed and
      directionally cloned (Scorv site is destroyed upon
      cloning). Average insert size 1.68 kb. Library was
      constructed by (Invitrogen). Note: this is a NIH_MGC
      Library."
  ORIGIN
    Query Match      30.7%; Score 297.4; DB 14; Length 905;
    Best Local Similarity 95.9%; Pred. No. 4.7e-59;
    Matches 327; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
  QY 1 ATGCTTCAACATCCAGTCTTCGGTACAGACTGACACCAATCAACGAGCTGAGGAG 60
  DB 390 ATGGATTCAACATCCAGTCTTCGGTACAGACTGACACCAATCAACGAGCTGAGGAG 449
  QY 61 ACTCTTCTCTAAGACAGACCTTGTGCTTCAAGGGCTGACGTGCAATCGCTTCCCTTGTTC 120
  DB 450 ACTCTTCTCTAAGACAGACCTTGTGCTTCAAGGGCTGACGTGCAATCGCTTCCCTTGTTC 509
  QY 121 GCGCTGACAGAAACGGGTTGTCTTCTGCTCTCTGGCTGCGCATGCGCAGAACGCT 180
  DB 510 GCGCTGACAGAAACGGGTTGTCTTCTGCTCTCTGGCTGCGCATGCGCAGAACGCT 569
  QY 181 GTCCTCATCTCATCTCTCAACCTGGTGGCGGCGCACTTCTCTCTCTTACGCGCCACATT 240

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Db 570 GTCTCCATCTACATCCTCAACCTGTCGCGCGCGACTTCCTCTCTTTAGCGGCAACATT 629
Qy 241 ATATGTTCCGCGCTTACGCTCATCAATAT-CCGCCATCCCATCTCCAAAATCCTCAGTCC 299
Db 630 ATACGTTCCGCGTTACGCTCTCAATATCCGCCATCCCTTCACAAAATCCTCAGTCC 689
Qy 300 TGTG--ATGACCTTTCCTACTTTATAGGCTTAAGCATGCT 338
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RESULT 12
LOCUS B1828553
DEFINITION B1828553 618 bp mRNA linear EST 04-OCT-2001
        60307843F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170163 5',
        mRNA sequence.
ACCESSION B1828553
VERSION B1828553.1 GI:15940103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
        National Institutes of Health, Mammalian Gene Collection (MGC)
        Unpublished (1999).
AUTHORS Contact: Robert Strausberg, Ph.D.
        Email: c9apbs@mail.nih.gov
        Tissue Procurement: Life Technologies, Inc.
        cDNA Library Preparation: Life Technologies, Inc.
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
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                /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: EcoRV (destroyed); RNA source normal medulla from
                anonymous male age 27. Library is oligo-dT primed and
                directionally cloned (EcoRV site is destroyed upon
                cloning). Average insert size 1.3 kb, insert size range
                0.9-3 kb. Library is normalized and enriched for
                full-length clones and was constructed by C. Gruber
                (Invitrogen). Research Genetics tracking code 013. Note:
                this is a NIH_MGC Library."
ORIGIN
Query Match 29.5%; Score 285.6; DB 12; Length 618;
Best Local Similarity 74.5%; Pred. No. 2.4e-56;
Matches 395; Conservative 0; Mismatches 114; Indels 21; Gaps 2;

Qy 1 ATGGATTCACCATCCAGCTTGGTACAGACTGACACCAATCAACGGACGTGAGGAG 60
Db 89 ATGGATTCACCAACCCCGCGCTGGGGAAACAGAAATACACAGTGAATGGAAATGACCAA 148
Qy 61 ACTCCT-----TGCTACAGCAGACCTTCAGCTTTCACGGGCTCAGCTGCATCGTT 111
Db 149 GCCTTCTTCTGTTTGTGGCAGGAGACCCGTGATCCCGGTCTTCTGTATCTTTTCATT 208
Qy 112 TCCTTGTCCGCTGACGAGAACCGGTTGTGCTCTGCTCTGGCTGGCGATGGCG 171
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Qy 172 AGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGCGCGACTTCCTCTTCTTAGC 231
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Qy 232 GGCCACATATATGTTGCGCGGTACCGCTCATCAATATCGGCATCCCATCCCAAAA-- 289
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Qy 290 -----TCCTCAGTCTGTGATGACCTTTCCCTACTTTATAGGCCCTTAAGCATGCTG 339
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Qy 340 AGGCCCATCAGCACCGAGCGCTCCCTGTGCTCATCTCTGCGCCATCTGGTACCACTGCCGC 399
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Qy 400 CGCCCCAGATACCTGTGCATCGGTTCATGTGTGCTCTCTGCGCCCTGCTGCTGCTGCGG 459
Db 509 CGCCCCAGACACCTGTGCAGGGTCTGTGCTGCTCTCTGCGCCCTGCTGCTGCTGCTG 568
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RESULT 13

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LOCUS BY741352
DEFINITION BY741352 RIKEN full-length enriched, B16 F10Y cells Mus musculus
        cDNA clone G370060H08 5', mRNA sequence.
ACCESSION BY741352
VERSION BY741352.1 GI:27166203
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FEATURES

source

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    /clone_lib="NIH_MGC_119"
    /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
    Site 2: EcoRV (destroyed); RNA source normal medulla from
    anonymous male age 27. Library is oligo-dT primed and
    directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.3 kb, insert size range
    0.9-3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 013. Note:
    this is a NIH_MGC Library."

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ORIGIN

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Query Match 29.5%; Score 285.6; DB 12; Length 618;
Best Local Similarity 74.5%; Pred. No. 2.4e-56;
Matches 395; Conservative 0; Mismatches 114; Indels 21; Gaps 2;

Qy 1 ATGGATTCACCATCCAGCTTGGTACAGACTGACACCAATCAACGGACGTGAGGAG 60
Db 89 ATGGATTCACCAACCCCGCGCTGGGGAAACAGAAATACACAGTGAATGGAAATGACCAA 148
Qy 61 ACTCCT-----TGCTACAGCAGACCTTCAGCTTTCACGGGCTCAGCTGCATCGTT 111
Db 149 GCCTTCTTCTGTTTGTGGCAGGAGACCCGTGATCCCGGTCTTCTGTATCTTTTCATT 208
Qy 112 TCCTTGTCCGCTGACGAGAACCGGTTGTGCTCTGCTCTGGCTGGCGATGGCG 171
Db 209 GCCTTGTGGGCTGGTAGGAAACGGGTTGTGCTCTGCTCTGGCTTCGGCTTCGGATGGCG 268

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TITLE

JOURNAL

MEDLINE

FURNED

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic

/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Stimulated peripheral blood leukocytes 82"
/note="Organ: circulatory system; Vector: pME18S-FL3;
Site 1: XhoI; Site 2: XhoI; The library was prepared from
polyA+ RNA from equine peripheral blood leukocytes
isolated from a healthy adult horse. The leukocytes were
stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 28.9%; Score 279.8; DB 14; Length 783;
Best Local Similarity 68.3%; Pred. No. 6.1e-55;
Matches 424; Conservative 0; Mismatches 182; Indels 15; Gaps 2;
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DB 150 ATGAATCCGAATGTACAGGCTGGGGACCAAACTCACACGACTGACCAACACGAGTCC 209
QY 61 ACTCCT--TGCTACAGCAGACCTGAGCTTCCAGGGCTGACGTCATCTGTTCCCTT 117
DB 210 CTCCTTAATGTACAGAGACCGTGTATCCAGGCCCTGCTACCTTACCATTCGCCCTG 269
QY 118 GTCGGCTGACAGAAACGGGTGTGTCTGTGCTGCTGTGGGTGCGCATGCGAGGAAAC 177
DB 270 GTCGGGTGGCAGGAAACGGGATTTGCTCTGTGATCTGCGCTTCCACATGCGGAGAAC 329
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DB 450 AGCATCTTCATCATCTGTGTGAATTTGCTTCTTTCGAGGCTGAGTATTTCTACCGCC 509
QY 346 ATGAGCAGCGAGCGCTGCTGCTCATCTGTGCGCCCATCTGTGATCACTGCGCGCGCC 405
DB 510 ATTAGCACTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569
QY 406 AGATACCTGTCATCGGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465
DB 570 AACACATCACTATGTCATATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629
QY 466 CTGAGTGGATGTTCTGTGACTTCTGCTGTTAGTGTGCTGATTTCTGTTTGTGTAACG 525
DB 630 CTGAACAGGTACTACTCGGCTTCTGTACAGACATTTGAGGATGTTGTTGTTGTTGTT 689
QY 526 TCAGATTTCATTACAAACCGGTGCTGTTTATTTTATGTTGTTGTTGTTGTTGTTGTTG 585
DB 690 TCATATTTTCCATATGCAAGTGGCTGACTTTTATTTGTTGTTTCTCTCGTCCAGC 749
QY 586 CTGCTCTGCTGTGAGGATT 506
DB 750 ATAGCCCTGTGTTCAAGATT 770

RESULT 15
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DEFINITION DXFZp86K2036_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION AL705589
VERSION AL705589.1 GI:19688944
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 515)
AUTHORS Wambutt R., Heubner D., Mewes W., Weil B. and Wiemann S.
TITLE EST (Wambutt R., Heubner D., Mewes W., Weil B. and Wiemann S.)
JOURNAL Unpublished (1999)
COMMENT CONTACT: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 5' sequence available.
This clone (DXFZp86K2036) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
Location/Qualifiers
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cDNA-collection"

ORIGIN

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DB 316 ATGGATCCCAACCGTCCAGTCTTGGGTACAAAACTGACACCAATCAACGAGCGTGAGGAG 257
QY 61 ACTCCTTGTACAGCAGACCGCTGAGCTTACGCGGCTGACGTGATGTTCCCTTCTC 120
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DB 196 GGAATGACAGGAAACCGGTTGTGCTTCTGGCTCTTGGGCTGCCGATGCGAGGAACGCT 137
QY 181 GTCTCCATCTACATCTCAACCTGTCGCGGCGGACTTCTCTCTTCTTCTTCTTCTTCT 240
DB 136 GTCTCCATCTACATCTCAACCTGTCGCGGCGGACTTCTCTCTTCTTCTTCTTCTTCT 77
QY 241 ATATGTTGCGCGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCTAGTCT 300
DB 76 ATAGTTGCGCATTTAGCGCTCATCAATATCCGCCATCTCATCCGAAAATCTCTCTTCT 17
QY 301 GTGATGACCTTTCCTT 316
DB 16 GTGATGACCTTTCCTT 1

Search completed: July 4, 2004, 07:21:43
Job time : 3097 secs